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1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
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Best Local Similarity 100.0%; Pred. No. 8.7e-138;
Matches 156; Conservative 0; Mismatches 0;
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STATE: MA
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Sequence 16, Appli
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                                                                                                                                                                                                                                                                                      ....TRGSNHARIDAAEGPSDIPD 156
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Compugen Ltd.
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US-08-366-511A-2
US-08-383-274-2
US-08-381-918A-2
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US-08-389-981-2
US-08-589-981-2
US-08-589-981-2
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US-08-384-116A-24
US-08-384-116A-24
US-08-384-116A-24
US-08-384-116A-24
US-08-384-116A-24
US-08-487-033-2
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US-08-486-047-2
US-09-115-252-2
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                                                                                                                                                  October 31, 2001, 07:09:53;
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                 GenCore version
Copyright (c) 1993 - 2000
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    protein search, using sw model

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Gapop 60.0 , Gapext 60.0
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Perfect score:
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                                                                                                         OM protein
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Maximum DB
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GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Depinho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                   Sedinence Sedine
          Sequence
US-08-487-033-14
US-08-480-810-14
US-08-848-251-14
US-08-86-047-14
US-09-120-130-14
US-09-120-124-14
US-09-120-129-14
US-09-120-129-14
US-09-120-129-14
US-09-120-139-14
US-09-120-139-14
US-09-120-139-14
US-09-120-139-14
US-08-120-139-14
US-08-120-139-14
US-08-120-139-14
US-08-120-138-14
US-08-581-918A-37
US-08-581-918A-38
US-08-581-918A-38
US-08-581-918A-38
US-08-581-918A-38
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NAME: Vincent, Matthew P.
REGISTATION UNDERS: 36,709
REFERENCE/DOCKET NUMBER: 621-001CP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/627,610
FILING DATE: 04 APR-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08627610
Patent No. 5919997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 amino acids
          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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Sequence

Length 156; Indels a

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USA
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COUNTRY:
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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLFVDLAEE 120 | ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLFVDLAEE 120 | ELLLHGAEPNCADPATLTFYHDAAREGFLDTLVYLHRAGARLDVRDAWGRLPVDLAEE 120 |
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                                                                                                                                                                                                                                                                          GEMERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: BOSLON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 156;
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100.0%; Pred. No. 8.7e-138;
Live 0; Mismatches 0;
                                                                                     121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                             121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMNUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (617) 227-7401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                 Sequence 2, Application US/08306511A
Patent No. 5962316
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Serrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Greacory I.
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amino acid
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Matches 156; Conservative
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US-08-306-511A-2
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US-08-893-274-2
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Patent No. 5968821
GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Manuel
APPLICANT: Cell-Cycle Regulatory Proteins, TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, TITLE OF INVENTION: and Uses Related Thereto NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 156; DB 2; I ilarity 100.0%; Pred. No. 8.7e-138; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-WAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APRIL-1994
PRIOR APPLICATION UNBER: US 08/154,915
FILING DATE: 18-WOVEMBER-1993
PRIOR APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-WOVEMBER-1993
PRIOR APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DECEMBER-1992
PRIOR APPLICATION NUMBER: 17-DECEMBER-1992
FILING DATE: 17-DECEMBER-1992
APPLICATION NUMBER: 18-07/963,308
APPLICATION NUMBER: 18-07/963,109
APPLICATION NUMBER: 18-07/963,308
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REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
                                                                                                                                                                                                                                                                                                                                                     LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02109
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INCEMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 156 amino acids
amino acid
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Matches 156; Conserv
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; Sequence 2, Application US/08893274

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 31, 2001, 07:10:53; Search time 14.49 Seconds

(without alignments)

#20.099 Million cell updates/sec

Title: US-09-016-869A-2

Perfect score: 156
Sequence: 1 MDPAAGSSMEPSADWLATAA......TRGSNHARIDAAEGPSDIPD 156

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 219241 seqs, 76174552 residues

| Size: 0
| size: 0
```

Post-processing: Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Fred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Des	cyclin dependent k CDK4 inhibitor p14 p151NK4b mouse gene p151NK4b prot p161NK4a mouse form (III) ABC tra hypothetical prote genome polyprotein genome polyprotein hypothetical prote ORP3 protein - Orf cyclin-dependent k CDK4/CDK6 inhibito cyclin-dependent k cDK4/CDK6 inhibito cyclin-dependent k probable nicotinam alcohol dehydrogen	
\mathbf{S}	JEOU41 1578479 1578479 157845 157845 157845 157845 157320 174347 444212 MNWWHE MNWWHE MNWWHE A4212 A70792 A70792 A51379 A51379 A51379 A51379 A51374 A75374 A	
DB		
Length	158 138 138 140 167 167 168 168 168 168 168 168 168 168 168 168	
% Query Match	7 4 6 7 4 7 4 7 4 4 4 4 4 4 4 4 4 4 4 4	
Score	1 1 2 4 8 8 8 8 8 6 7 7 7 7 7 7 7 7 7 7 7 7 7 7	
Result No.	22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	

ALLGNMENTS

	A,Status: translation not shown; translated from GB/EMBL/DDBJ A,Molecule type: DnA A,Roblecule type: DnA A,Residues: 51-152 <kam> A,Residues: 51-152 <kam> A,Cross-references: GB:S69804; NID:9546272; PIDN:AAD14048.1; PID:94261748 C;Comment: This protein inhibits the activity of cyclin Dl/CDK4 and cyclin Dl/CDK6 ki C;Genetics: A;Gene: GBB:CDKN2A; CDK41; MLM; P16; INK4; MTS1; CMM2; CDKN2 A,Cross-references: GBB:33532; OMIM:600160 A;Map position: 9p21-9p21</kam></kam>	C. Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol C. Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol C. Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
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Gispecies: Ratus sp. (fat)
Cispecies: 152720
Richapek, Dr.; Serrano, M. Beach, D.; Trono, D.; Walker, C.L.
Cancer Res. 55, 1607-1612, 1995
A;Title: Association of rat pl5INK4B/pl6INK4 deletions with monosomy 5 in kidney epit
A;Reference number: 152720; MuID:95228036
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 152720
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-41 cRES>
A;Cross-references: GB:S77734; NID:9998711
C;Genetics: 1-4
A;Genetics: pl5INK4B
A;Genetics: pl5INK4B
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
                                                                                                                                                                                                                                                                                                                                                                                                        PISTRAGE
PISTRICAD - mouse
pl51NK4b - mouse
pl51NK4b - mouse
c;Species: Mus sp. (mouse)
c;Species: Mus
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
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p16INK4a - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C;Accession: 158352
R;Quelle, D.E.; Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H
Gaps
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Pred. No. 1.4e-39;
0; Mismatches 0;
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Pred. No. 2.7e-26;
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100.0%; Pre
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Best Local Similarity 100.0%; P
Matches 48; Conservative 0;
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                                                                                                                                           109 AWGRLPVDLAEE 120
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                           Q_{Y}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitor pl4(INK4B/MTS2) - human ternate names: CDK6-associated protein pl5(INK4B); cyclin-dependent kinase inhibitor c)specias: Homo sapiens (man) c. Saccias: Jamar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jul-2000 C; Accession: B55479; S47593; I81183; I52713 R; Guan, K.L.; Jankins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G.; Genes Dev. 8, 2939-2952, 1994 A; Illie: Growth suppression by pl8, a p16(INK4/MTS1)- and p14(INK4B/MTS2)-related CDK6 in A; Reference number: A55479; MuID:95095079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 St
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Title: A cell cycle regulator potentially involved in genesis of many tumor types. A:Reference number: 159585; MUID:94204645
A:Accession: 181183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: B237.16; ACCESSION: B237.16; ACCESSION: B237.16; A; Residues: 1-138 < CGUA.
A; Residues: 1-138 < CGUA.
A; Residues: 1-138 < CGUA.
A; Cross-references: GE-U17075; NID: 96397.15; PIDN: AAC50075.1; PID: 96397.16
A; Experimental source: HeLa cells
A; Hannon, G.J.; Beach, D.
Astrille: p15(IRK4B) is a potential effector of TGF-beta-induced cell cycle arrest.
A; Reference number: S47593; MUID: 94359613
A; Reference number: S47593; MUID: 94359613
A; Residues: 1-19; TPV, 22, 24-31, HSW', 35-138 < HAN>
A; Residues: 1-19; TPV, 22, 24-31, HSW', 35-138 < CGUA.
A; Residues: Hacar cells
A; Cross-references: GB: L36844; NID: 9556197; PIDN: AAA50282.1; PID: 9556198
A; Cross-references: Hacar cells
A; Experimental source: Hacar cells
A; Experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        atus: translation not shown; translated from GB/EMBL/DDBJ lecule type: DNA A; Residues: 53-138 < KAMA A; Cross-references: GB:S69805; NID:9546273; PIDN:AAD14049.1; PID:94261749 R; Jen, J; Harper, J.W.; Bigner, S.H.; Bigner, D.D.; Papadopoulos, N.; Markowitz, Cancer Res. 54, 635-6358, 1994 A; Title: Deletion of p16 and p15 genes in brain tumors. A; Reference number: 152713; MUID:95079408 A; Accession: 152713
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Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                            96 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                                                                                           96 VLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIP 155
                                                                                              Gaps
                                                                                                                                                                                                                                         36 ALPNAPNSYGRRPIQVMMYGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV 95
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                                                                                                                                                                                        36 ALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLV
                                                                                              ;
0
         Length 156;
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    DB 2; Le
3.4e-111;
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46.2%; Score 72; DB 2; L
Best Local Similarity 100.0%; Pred. No. 3.9e-63;
Matches 72; Conservative 0; Mismatches 0;
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A;Molecule type: DNA
A;Residues: 1-52 <RES>
    Query Match 77.6%; Score 121; DE Best Local Similarity 100.0%; Pred. No. 3.4 Matches 121; Conservative 0; Mismatches
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| SUMMARIES | ription        | MAN P42771 homo sapien | P42772 homo | E P55271 mus m |      | P51480 |     | 003495       | P29324 | 004610 |            |      | 060773 |             | 032028 | P23236 | P22246 | P07161 | P12854 | P27581 | P25720 | P23237 | P09369 | P07160 | P25721 | P24267 | 699000 | P21518 | P22245 | P51551 | P51549 | P21898      | MM Q00671 drosophila |
|-----------|----------------|------------------------|-------------|----------------|------|--------|-----|--------------|--------|--------|------------|------|--------|-------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|-------------|----------------------|
| SUMM      | DB ID          | 1 CDN2 HUMAN           |             |                |      | _      |     | 1 POLN_HEVME |        |        |            | CDN7 | -      | 1 GPH_RHOSH | MIM .  | ADH1   | ADH1   |        |        |        |        |        |        |        |        |        |        | -      |        |        | ADH    | 1 ADH_DROHE | 1 ADH_DROMM          |
|           | Length         | 156                    | 138         | 130            | 130  | 167    | 171 |              |        |        |            |      |        |             |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        |        | 253         |                      |
| d         | Query<br>Match |                        |             |                | 23.1 |        |     | 5.1          | 5.1    | 5.1    | 5.1        | 4.5  | 4.5    | 4.5         | 4.5    | 4.5    | 4.5    | 4.5    | 4.5    | 4.5    | 4.5    | 4.5    |        |        |        |        |        |        |        |        | 4.5    | 4.5         | 4.5                  |
|           | Score          | 12                     | 72          | 48             | 36   | 19     | 14  | 89           | 8      | 80     | <b>6</b> 0 | 7    | 7      | 7           | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7      | 7           | 7                    |
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| RESULT     | RESULT 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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| G          | CDN2_HUMAN STANDARD; PRT; 156 AA.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| AC 3       | P42771; 015191;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 5 5        | 01-NOV-1995 (KRI. 31, Credted)<br>16-THI-1998 (PD) 36 Tast sequence undate)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
|            | 1. John 1970 (Not.) John Mark Advance Aproxie)<br>01-071-2000 (Rel 40. Last annotation undate)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| DE         | CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK41) (P16-INK4) (P16-INK4A)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| DE         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| CN         | CDKN2A OR CDKN2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| OS<br>O    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| ပ<br>ဝ (   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| 2 8        | Mammatla; butherla; Frimates; Catarrnin; Hominidae; Homo.<br>Month moutholder                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| <b>Y</b> 2 | NCBI_10XID=9000;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 0.00       | LA1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| RX         | MEDLINE=94081956; Pubmed=8259215;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| RA         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RT         | "A new regulatory motif in cell-cycle control causing specific                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| RŢ         | inhibition of cyclin D/CDK4.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| RE         | Nature 366:704-707(1993).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| KN.        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| RP         | SEQUENCE OF 51-152 FROM N.A.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| X          | MEDLINE=94Z04645; PubMed=8153634;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| RA         | Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| ¥ 4        | Tavilgian D.V., Stockett E., Day R.S. 111, Johnson B.E., Skolnick M.H.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| Z E        | SACTULES A.M                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| RT         | types. ":                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| RI         | 27 F 20 264 - 446 (1994)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
| Z Z        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| d d        | SECTIENCE OF 1-20 FROM N A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| X X        | MEDITURE 96182088: PubMed=8622687:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| RA         | Hara E., Smith R., Parry D., Tahara H., Stone S., Peters G.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| RT         | "Regulation of p16CDKN2 expression and its implications for cell                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| RT         | immortalization and senescence.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| RL         | Mol. Cell. Biol. 16:859-867(1996).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| RN         | [4]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| RP         | X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| RX         | MEDLINE=98421670; PubMed=9751050;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| RA         | Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| RT         | "Structural basis for inhibition of the cyclin-dependent kinase cake                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| RŢ         | by the tumour suppressor plbINK4a.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| Z :        | Nature 395:23/-243(1998).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| X C        | DEVITED ON METANOMA VARETANING                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| ያ<br>ያ     | REVIEW ON MELANDAM VARIANIS.<br>MEDITATE AG377761. DibMad=8783570.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| NA<br>PA   | MINISTERNIA OCCUPATION TO TRANSPORT TO THE TABLE OF THE T |
| E E        | TODAN DESTATIONS in melanoma":                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| RL         | Cancer Surv. 26:115-132(1996).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| RN         | [9]                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| RP         | REVIEW ON VARIANTS.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| RX         | MEDLINE=96303699; PubMed=8723678;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| RA         | Smith-Soerensen B., Hovig E.;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| RT         | "CDKN2A (p16INK4A) somatic and germline mutations.";                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| RL         | Hum. Mutat. 7:294-303(1996).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

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 Hayashi N., Sugimoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
"Somatic mutations of the MTS (multiple tumor suppressor) 1/CDK41
(cyclin-dependent kinase-4 inhibitor) gene in human primary non-small
                                                                                                                                            MEDLINE-95078916; PubMed-7987387; Hussubsian C.J., Struewing J.P., Goldstein A.M., Higgins P.A.T., Ally D.S., Sheahan M.D., Clark W.H. Jr., Tucker M.A., Dracopoli N.C.; "Germline pl6 mutations in familial melanoma.";
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                                                                                                                              VARIANTS MELANOMA THR-49; SER-71; PRO-87; TRP-101; ASP-126 & THR-148
MEDLINE-95078916; Pubmed-7987387;
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                                                                                                                                                                                                                         VARIANTS SQUAMOUS CELL CARCINOMA (SCCA) SER-127 AND CYS-144. MEDILNE-95060835; PubMed-7970734; Zhou X., Tarmin L., Yin J., Jiang H.-Y., Suzuki H., Rhyu M.-G., Abraham J.M., Meltzer S.J.; "The MYSI gene is frequently mutated in primary human esophageal tumors.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walker G.J., Hussussian C.J., Flores J.F., Glendening J.M., Haluska F.G., Dracopoll N.C., Hayward N.K., Fountain J.W.; "Mutations of the CDKNZ/pl6INK4 gene in Australian melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Mutations associated with familial melanoma impair {\tt pl6INK4} function.";
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Biochem. Biophys. Res. Commun. 202:1426-1430(1994).
              VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).
MEDLINE=94338359; PubMed=8060323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Genet. 4:1845-1852(1995).
                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95188190; PubMed=7882351;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS FAMILIAL MELANOMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                    WOSKBANT PANCKEATIC CARCINOMA CYS-146.
MOSKBALUK C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L.,
Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.;
"Novel germline pl6INK4 allele (Asp145Cys) in a family with multiple pancreatic carcinomas.";
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A -> P (IN A LUNG TUMOR AND MELANOMA).
/FIId=VAR_OOL410.
A -> S (IN A BILLARY TRACT TUMOR).
/FIId=VAR_OOL411.
G -> D (IN A PANCER).
                                                                                                                                                                                                                                                                                Gretarsdottir S., Olafsdottir G.H., Borg A.;
Five novel somatic CDKNZ/P16 mutations identified in melanoma,
glioma and carcinoma of the pancreas.";
Hum. Mutat. 12:212-212(1998).
-!- FUNCTION: INTERACTS STRONGIN WITH CDK4 AND CDK6. INHIBITS ITS
ABLITAY TO INTERACTY MITH CYCLINS D. COULD ACT AS A NEGATIVE
REGULATOR OF THE PROLIFERATION OF NORMAL CELLS.
-!- SUBUNTY: HETERODIMER WITH CDK4 OR CDK6.
-!- SUBUNTY: HETERODIMER WITH CDK4 OR CDK6.
-!- DISEASE: CDKNZA MUTATIONS ARE INVOLVED IN TUMOR FORMATION IN A
WIDE RANGE OF TISSUES.
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/FILG-VAR_001408.
L -> P (IN A BILIARY TRACT TUMOR AND
FAMILIAL MELANOMA).
                         В.
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Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J., Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets Hum. Mol. Genet. 7:941-941(1998).
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/FITG=VAR_001412.
R -> C / TTT
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E -> D (IN A BILT
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PROSITE: PS50297; ANK_REP_REGION: 1.
Cell cycle; Anti-concepen; Repeat; AN Polymorphism; 1.-Fraumeni syndrome; 3.
REPEAT 11
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ANK 4.
D -> E
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EMBL, U12820; AAB60645.1; --
EMBL, U12819; AAB60645.1; JOINE
EMBL, U12819; AAB60645.1; JOINE
EMBL, S69804; AAD14048.1; --
EMBL, S49184; AAD14048.1; --
PDB: 1B17; 16-FEB-99.
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Post-processing: Listing first 45 summaries

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### SUMMARIES

| Description                   | neines omod 20aa00 | Ogomfo cania famil |        |        | 054846 mis misculu | 09x10x mis spretus | Ogding mis missing | O9tsv1 sus scrofa | Oguph7 bomo sabjep | 095440 homo sanjen | Oftewn Survey | Ogowh4 mis misculu | O9x1C2 mis spretus | Ogroza mar offices | 089088 min sim 880680 | 3      | 200    | 2      | Snu    |  |
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| %<br>Query<br>Match Length DB | 106                | 81                 | 86     | 102    | 98                 | 86                 | 86                 | 103               | 36                 | 116                | 86            | 112                | 113                | 159                | 168                   | 168    | 113    | 113    | 113    |  |
| %<br>Query<br>Match           | 67.9               | 34.6               | 32.7   | 32.7   | 30.8               | 30.8               | 30.8               | 30.1              | 20.5               | 20.5               | 16.7          | 12.2               | 12.2               | 12.2               | 12.2                  | 12.2   | 11.5   | 11.5   | 11.5   |  |
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## ALIGNMENTS

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| RESULT 1<br>Q9NP05 |  | 01-OCT-2000 (TrEMBLrel. | 01-MAR-2001 (TrEMBLrel, 16, |  | OS Homo sapiens (Human). | OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi: | Mammalia; Eutheria; Primates; | RN [1] | RP SEQUENCE FROM N.A. | RX MEDLINE=94203288; PubMed=8152487; | RA Nobori T., Miura K., Wu D.J., Lois A., Takabayashi K., Carson D.A.: | RT "Deletions of the cyclin-dependent kinase-4 inhibitor gene in multiple | RT human cancers."; | RL Nature 368:753-756(1994). | DR EMBL; S69824; AAD14050.1; | DR EMBL; S69822; AAD14050.1; JOINED. | DR InterPro; IPR002110; | DR Pfam; PF00023; ank; 1. | DR PROSITE: PS50297: ANK REP REGION: 1 |  | Query Match 67.9%; Score 106; DB 4; Length 106; |    | QY 51 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 110 | Db 1 VMMGSARVAELTITIGAEDNCADDATTTPUTDATTTTTTTTTTTTTTTTTTTTTTTTTTTT |  |
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Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.;
"Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A)
and p15(MTS2/CDKN2B).";
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; B4010808; BaA33541.1; -.
HSSP; P55273; 1BDB.
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Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
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Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                    Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.7%; Score 51; DB 6; Length 86; 100.0%; Pred. No. 2.2e-40; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                 Venkatraj V.S., Mayor J., Modiano J.F.;
"Role of p16/Ink4 a in familial canine cancers.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF234176; AAG01087.1;
                                                                                                                                                                                                                                     81 81 81 81 823 0E39D8D805BEACOF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AA; 9340 MW; A59FF0193290E867 CRC64;
                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINSE 4/6 INHIBITOR-A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                  34.6%; Score 54; DB 6; Le
100.0%; Pred. No. 3.1e-43;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  86 AA
                         81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002110; -.
Pfam: PF00023; ank; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Conservative
                                                                                                                                                                                                                                                                                                            54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                         PRELIMINARY;
                                                                                               Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID-9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9685;
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SEOUENCE
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SEQUENCE
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                                       Q9GMF2;
                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XS52
                         Q9GMF2
                                                                                                                                                                                                                                                                                                                                                                                                                               09XS52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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              09GMF2
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Justicerpus, Cro K., Setoguchi A., Minehata K., Yazawa M., Endo Y., Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.; "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKN2A) and p15(MTS2/CDKN2B)"; the feline genes p16(MTS1/CDKN2A) and p15(MTS2/CDKN2B)"; the EMBL, AB010807; BAA33540.1; -. HSSP; P42771; 1B17.
InterPro: IPR002110; -. Pfam; PF00123; ank; 3.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                            P16/CDKN2A/MTS1 (FRAGMENT).
Felis silvestris catus (Cat).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/G5,
STRAIN-C57BL/G5,
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 787013460; ABB94534.1; -...
InterPro; IPR002110; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT).
CDKN2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26399FF21359F35D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 VAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86 AA; 9237 MW; 0499DB26144FB6DF CRC64;
                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.8%; Score 48; DB 11; I
100.0%; Pred. No. 1.5e-37;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.7%; Score 51; DB 6; Lv 100.0%; Pred. No. 2.5e-40; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50297; ANK_REP_REGION; 1.
       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      102 AA; 10824 MW;
01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RESULT

4

RESULT 09XS51

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2001, 07:06:13; Search time 19.51 Seconds (without alignments) 484.743 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                       156
1 MDPAAGSSMEPSADWLATAA......TRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2: SIDSB/gcgdata/geneseq/geneseqp/AA1980 DAT:*
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3: SIDSB/gcgdata/geneseq/geneseqp/AA1982 DAT:*
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3: SIDSB/gcgdata/geneseq/geneseqp/AA1991 DAT:*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412676 seqs, 60623988 residues
                                                                                                                                OM protein . protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Listing first 45 summaries
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                  US-09-016-869A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_0601:*
                                                                                                                                                                                                      October 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

|   |        | Description        |     | Cell-cycle requiat | HIMAN TAK-A protei | Himan coll cycle r | CDK inhihitory fun | Human n27-n16 fine; | Human M3 protoin o | Antingo iforetimo | Andiodopoeie inhih | Multiple tumour su | Human multiplo tum | Tabibitor of eveli | 110 TO 1001011111 |
|---|--------|--------------------|-----|--------------------|--------------------|--------------------|--------------------|---------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| ! |        | ID                 |     | AAKBSII6           | AAY24741           | AAY88354           | AAW23534           | AAW95094            | AAY97526           | AAY96041          | AAY96068           | AAR81701           | AAR80940           | AAR53401           |                   |
|   |        | DB                 | 1 . | Q T                | 20                 | 21                 | 18                 | 20                  | 21                 | 21                | 21                 | 16                 | 16                 | 15                 |                   |
|   |        | Watch Length DB ID |     | 9CT                | 156                | 156                | 391                | 391                 | 391                | 391               | 391                | 148                | 148                | 151                |                   |
| æ | Query  | Match              |     | 7007               | 100.0              | 100.0              | 98.1               | 98.1                | 98.1               | 98.1              | 98.1               | 94.9               | 94.9               | 94.9               |                   |
|   |        | Score              | 731 | OCT.               | 156                | 156                | 153                | 153                 | 153                | 153               | 153                | 148                | 148                | 148                |                   |
|   | Result | No.                | -   | 4                  | 7                  | e                  | 4                  | Ŋ                   | 9                  | 7                 | 80                 | σ                  | 10                 | 11                 |                   |

| Tumour suppressor | Ε        | acid segu |          | n mul    | Human MTS1 protein | ū        | Human cyclin depen | Human cyclin depen |          | Human multiple tum |          |           | Protein encoded by | Human Multiple Tum | Human W9 protein s | Antiproliferative | Angiogenesis inhib |          | Ω.       | Antiproliferative | Angiogenesis inhib | Truncated p27/p16 |          | 44       | Angiogenesis inhib | Secretable angioge | Truncated p27/p16 |          | Antiproliferative | Angiogenesis inhib | CDK inhibitory fus | Human p16p27 fusio | Human p16p27 fusio |
|-------------------|----------|-----------|----------|----------|--------------------|----------|--------------------|--------------------|----------|--------------------|----------|-----------|--------------------|--------------------|--------------------|-------------------|--------------------|----------|----------|-------------------|--------------------|-------------------|----------|----------|--------------------|--------------------|-------------------|----------|-------------------|--------------------|--------------------|--------------------|--------------------|
| AAW10627          | AAW19251 | AAW74549  | AAW40524 | AAW80524 | AAB15498           | AAY97524 | AAY96053           | AAY96067           | AAY92921 | AAY91102           | AAY59415 | AAY 54902 | AAB67334           | AAB36890           | AAY97522           | AAY96051          | AAY96078           | AAW95105 | AAY97534 | AAY96049          | AAY96076           | AAW95106          | AAY97535 | AAY96050 | AAY96077           | AAY96079           | AAW95103          | AAY97532 | AAY96047          | AAY96074           | AAW23536           | AAW95107           | AAW95096           |
| 18                | 18       | 19        | 19       | 20       | 21                 | 21       | 21                 | 21                 | 21       | 21                 | 21       | 21        | 22                 | 22                 | 21                 | 21                | 21                 | 20       | 21       | 21                | 21                 | 20                | 21       | 21       | 21.                | 21                 | 20                | 21       | 21                | 21                 | 18                 | 20                 | 20                 |
| 156               | 156      | 156       | 156      | 156      | 156                | 156      | 156                | 156                | 156      | 156                | 156      | 156       | 156                | 156                | 228                | 228               | 228                | 237      | 237      | 237               | 237                | 252               | 252      | 252      | 252                | 323                | 334               | 334      | 334               | 334                | 365                | 365                | 365                |
|                   |          | 77.6      |          |          | 77.6               |          |                    | 77.6               |          |                    |          |           |                    | 77.6               | 77.6               | 77.6              | 77.6               | 9.77     | 77.6     | ٠                 | 9.72               | •                 | •        | 77.6     | ٠                  |                    | 9.77              | •        | 77.6              |                    |                    | •                  | 9.77               |
| 121               | 121      | 121       | 121      | 121      | 121                | 121      | 121                | 121                | 121      | 121                | 121      | 121       | 121                | 121                | 121                | 121               | 121                | 121      | 121      | 121               | 121                | 121               | 121      | 121      | 121                | 121                | 121               | 121      | 121               | 121                | 121                | 121                | 121                |
| 12                | 13       | 14        | 15       | 16       | 17                 | 18       | 19                 | 20                 | 21       | 22                 | 23       | 24        | 25                 | 56                 | 27                 | 28                | 29                 | 30       | 31       | 32                | 33                 | 34                | 35       | 36       | 37                 | 38                 | 39                | 40       | 41                | 42                 | 43                 | 44                 | 45                 |
|                   |          |           |          |          |                    |          |                    |                    |          |                    |          |           |                    |                    |                    |                   |                    |          |          |                   |                    |                   |          |          |                    |                    |                   |          |                   |                    |                    |                    |                    |

### ALIGNMENTS

| RESULT<br>AAR851 | RESULT 1<br>AAR85116                                                  |
|------------------|-----------------------------------------------------------------------|
| QI<br>XX         | AAR85116 standard; Protein; 156 AA.                                   |
| Y Y              | AAPR5116.                                                             |
| ××               |                                                                       |
| DT               | 01-MAR-1996 (first entry)                                             |
| XX               |                                                                       |
| DE               | Cell-cycle requiatory protein p16.                                    |
| xx               |                                                                       |
| ΚW               | Cell-cycle regulatory protein p16; cyclin-dependent kinase inhibitor; |
| KE               | CCR; cancer; cell proliferation.                                      |
| XX               |                                                                       |
| 08               | Homo sapiens.                                                         |
| ××               |                                                                       |
| PN               | WO9528483-A1.                                                         |
| ××               |                                                                       |
| PD               | 26-OCT-1995.                                                          |
| XX               |                                                                       |
| PF               | 14-APR-1995; 95WO-US04636.                                            |
| XX               |                                                                       |
| PR               | 29-NOV-1994; 94US-0346147.                                            |
| PR               |                                                                       |
| PR               | 25-MAY-1994; 94US-0248812.                                            |
| PR               |                                                                       |
| XX               |                                                                       |
| PA               | (COLD-) COLD SPRING HARBOR LAB.                                       |
| XX               |                                                                       |
| ΡI               | Beach DH, Demetrick DJ, Hannon GJ, Serrano M:                         |
| XX               |                                                                       |
| DR               | WPI; 1995-373798/48.                                                  |
| DR               | N-PSDB; AAT02962.                                                     |
| ×                |                                                                       |
| ΡŢ               | New cell cycle regulating proteins bind to cyclin dependent kinase -  |

New cell cycle regulating proteins bind to cyclin dependent kinase

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sal Similarity
156; Conserv
                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA13096
                                                                                                                                                                                                                                                                  156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1993;
14-APR-1994;
25-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COLD-) COLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6043030-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beach DH,
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S.
Matches 156
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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0
                                                                                           The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was obtd. by expression of a cDNA clone (AA702962) isolated in a 2-hybrid screening assay. CCR p16 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      1 mdpaagssmepsadwlataaargrveevralleavalpnapnsygrrpigvmmmgsarva 60
                                                                                                                                                                                                                                                                                                                                                                  1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
and related nucleic acids, antibodies etc., used in diagnosis and
therapy of abnormal cell proliferation, degeneration etc.
                                                                                                                                                                                                                                                                                                                                                                                        INK-4; p16; p15; p18; p19; CDK4; cell cycle regulatory protein; transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.
                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                      Length 156;
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic mice with modified cell-cycle regulation
                                                                                                                                                                                                                                                                                        100.0%; Score 156; DB 16; 100.0%; Pred. No. 1.2e-141;
                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                         Claim 1; Page 76-77; 109pp; English.
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93US-0154915.
94US-0227371.
94US-0248812.
94US-0306511.
94US-0346147.
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                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 156; Conservative
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                                                                                                                                                                                                                                    156 AA;
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The present invention describes a transgenic mouse having germline and somatic cells which comprise an incorporated transgene that disrupts and inhibits the p16-TNK4-a gene leading to tumour susceptibility. Also described is a method of making a mouse and mouse embryonic stem cells a functionally disrupted p16-INK4-a gene which comprises transferring a transgene construct into embryonic stem cells of mouse and excorpt these into a mouse blastocyst and implanting the resulting chimeric blastocyst into a female mouse selecting offspring having an endogenous p16-IKK4-a gene allele. The transgenic mouse is useful for evaluating the carcinogenic potential or the anti-proliferative activity of a test compound. The present sequence represents the human INK4 protein p16 given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection; cell proliferation; differentiation; neoplasia; cancer; cell growth; cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory protein) in a diagnostic assay for identifying a cell at risk for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cell cycle regulatory protein p16 amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 156; DB 20;
Pred. No. 1.2e-141;
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY88354 standard; Protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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93US-0154915.
94US-0227371.
94US-0248812.
94US-0306511.
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95US-0497214.
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

October 31, 2001, 07:02:33 ; Search time 70.99 Seconds (without alignments) 167.393 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-016-869A-2 800 1 MDPAAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched: number of hits satisfying chosen parameters:

219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_68:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|           | Description         | cvclin dependent k | p - mouse | CDK4 inhibitor p14 | p16INK4a'- mouse | cyclin-dependent k | CDK4/CDK6 inhibito | cyclin-dependent k | CDK4/CDK6 inhibito | CDK6 inhibitor p18 | gene p15INK4B prot | ankyrin 2, neurona | -      | - 1    | ٦,     | ٦,     | Ę,    | potassium channel | death-associated p | potassium channel |        |        | 'n     | 'n     | ankyrin 3, long sp | -related | elegans ankyrin-re | ankyrin-related un | ankyrin-related un | probable ankyrin [ |
|-----------|---------------------|--------------------|-----------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|-------|-------------------|--------------------|-------------------|--------|--------|--------|--------|--------------------|----------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ID                  |                    | 178845    | B55479             | ന                | 573                | 5                  | B57378             | B57379             | A55479             | 152720             | S37431             | S37771 | 149502 | B35049 | A35049 | SJHUK | S62694            | 137275             | S23606            | T42714 | T42715 | T42713 | T42716 | A55575             | A57282   | ഥ                  | 534                | 1534               | D84448             |
|           | DB                  | 2                  | 7         | N                  | 7                | 7                  | ~                  | 7                  | ~                  | ~                  | 7                  | ď                  | 7      | 7      | ~      | 7      | П     | 7                 | _                  | ~                 | ~      | ~      | ~      | ~      | 7                  | ~        | ~                  | 7                  | ~1                 | 7                  |
|           | Length              | 156                | 130       | 138                | 167              | 164                | 166                | 166                | 168                | 168                | 41                 | 3924               | 1848   | 1862   | 1856   | 1880   | 1881  | 857               | 1423               | 838               | 1765   | 1940   | 1943   | 1961   | 4377               | 1786     | 1815               | 1867               | 2039               | 247                |
|           | &<br>Query<br>Match | 98.6               | 66.1      | 65.8               | 57.7             | 32.2               | 31.1               | 30.5               | 28.9               | 28.6               | 26.1               | 19.8               | 17.2   | 17.2   | 16.7   | 16.7   | 16.7  | 16.4              | 16.3               | 16.2              | 16.2   | 16.2   | 16.2   | 16.2   | 16.0               | 5.       | •                  | •                  | 15.9               | •                  |
|           | Score               | 789                | 529       | 526                | 461.5            | 258                | 249                | 244                | 231.5              | 228.5              | 209                | 158                | 137.5  | 137.5  | 133.5  | 133.5  | 133.5 | 131               | 130.5              | 130               | 130    | 130    | 130    | 130    | 128                | 127.5    | 127.5              | 127.5              | 127.5              | 126                |
|           | Result<br>No.       |                    | 7         | Э                  | 4                | Ŋ                  | Q                  | 7                  | 80                 | 6                  | 10                 | 11                 | 12     | 13     | 14     | 15     | 16    | 17                | 18                 | 19                | 20     | 21     | 22     | 23     | 24                 |          |                    |                    | 28                 |                    |

| notch4 - mouse | hypothetical prote | related to 26s pro | probable potassium | hypothetical prote | GA-binding protein | GA-binding protein | nuclear respirator | nuclear respirator | nuclear respirator | nuclear respirator | hypothetical prote | hypothetical prote | ankyrin – fruit fl | ankyrin-like prote | potassium channel |
|----------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|
| T09059         | T15888             | T50984             | D84650             | T23213             | C40858             | B40858             | C48146             | I38744             | 138743             | 138741             | T32930             | T43458             | T13940             | D82654             | T52046            |
| ~              | ~                  | ~                  | 7                  | 7                  | 7                  | 7                  | 7                  | 7                  | ~                  | 7                  | ~                  | 7                  | 7                  | 7                  | 7                 |
| 1964           | 209                | 237                | 888                | 476                | 347                | 382                | 347                | 348                | 360                | 395                | 1435               | 1031               | 1549               | 1058               | 828               |
| 15.6           | 15.6               | 15.1               | 15.1               | 15.0               | 14.8               | 14.8               | 14.7               | 14.7               | 14.7               | 14.7               | 14.6               | 14.6               | 14.5               | 14.4               | 14.2              |
| 125            | 124.5              | 121                | 121                | 120                | 118.5              | 118.5              | 117.5              | 117.5              | 117.5              | 117.5              | 117                | 116.5              | 116                | 115.5              | 114               |
| 30             | 31                 | 32                 | 33                 | 34                 | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                |

## ALIGNMENTS

| <br>RESULT 1 JE0141 Cyclin dependent kinase inhibitor - human N.Alternate names: CDK4 inhibitor p16(INK4A/MTS1); cyclin-dependent kinase inhibitor C;Species: Homo sapiens (man) C;Dete: 02-un-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <br>R.Huang, C.G.: Deng, W.: Fu, J.C. Chin. J. Biotechnol. 13, 105-107, 1997 A.Title: Molecular cloning and sequencing of P16 ink4 cDNA from hela cell. A.Recession: JE0141 A.Rocession: JE0141 A.Molecule type: mRNA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| <br>A; Experimental source: Hella cell A; Experimental source: Hella cell R; Okamoto, A.; Demetrick, D.J.; Spillare, E.A.; Hagiwara, K.; Hussain, S.P.; Bennett, Proc. Natl. Acad. Sci. U.S.A. 91, 11045-11049, 1994 A; Title: Mutations and altered expression of p16INK4 in human cancer. A; Reference number: 159268; MUID:95062202 A; Accession: 159268                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| <br>A.Status: translation not shown; translated from GB/EMBL/DDBJ A.Status: translation not shown; translated from GB/EMBL/DDBJ A.Status: translation not shown; translated from GB/EMBL/DDBJ A.Status: 1-152 < OKRA A.Residues: 1-152 < OKRA A.Ross-references: GB.L27211; NID:9558656; PIDN:AAA92554.1; PID:9558657 A.Note: the sequence is revised in GenBank entry HUMINK4X, release 113.0, PIDN:AAA925 B.Serrano, M.; Hannon, G.J.; Beach, D.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <br>Nature 360, 704-707, 1993 A)Title: A new regulatory motif in cell-cycle control causing specific inhibition of A)Title: A new regulatory motif in cell-cycle control causing specific inhibition of A)ACcession: S39359 A)Accession: S39359 A)Status: preliminary A)Molecule type: mRMP A)Molecule type: mRMP A)Molecule 4,00:34,00,000 A)A,001ecule type: mRMP A)A,001ecule t |
| <br>A.Note: this sequence is corrected in reference IS9268 R.Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Schence 264, 436-440, 1994 A.Title: A cell cycle regulator potentially involved in genesis of many tumor types. A.Reference number: IS9585; MUID:94204645                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <br>A.Status: translation not shown; translated from GB/EMBL/DDBJ A.Molecule type: DNA A.Residues: 51-152 KRM> A.Cross-references: GB:S69804; NID:9546272; PIDN:AAD14048.1; PID:94261748 C.Comment: This protein inhibits the activity of cyclin D1/CDK4 and cyclin D1/CDK6 ki C.Genetics: A.Genetics: A.G |
| <br>C; Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |

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A; Closs-Interestical Source: HaCaT Calls
R; Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Science 264, 435440, 1994
R; Kamb, A.; Gruis, N.A.; Weaver-Feldhaus, J.; Liu, Q.; Harshman, K.; Tavtigian, S.V.; Science 264, 435440, 1994
A; Title: A cell cycle regulator potentially involved in genesis of many tumor types. A; Reference number: 159585, MUID:94204645
A; Accession: 181183
A; Accession: 181183
A; Residues translation not shown; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 53-138 cKAM>A; Reference number: 152713; MUID:95079408
A; Title: Deletion of p16 and p15 genes in brain tumors.
A; Reference number: 152713; MUID:95079408
A; Recession: 152713
A; Molecule type: DNA
A; Residues: 1-52 cKES
A; Resid
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:Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
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R: Quelle, D. E.; Ashmun, R. A.; Hannon, G. J.; Rebberger, P. A.; Trono, D.; Richter, B. R: Quelle, D. E.; Ashmun, R. A.; Hannon, G. J.; Rebberger, P. A.; Trono, D.; Richter, B. A.; Title: Cloning and characterization of murine pl6INK4a and pl5INK4b genes.
A; Preference number: 158352; MUID:95380169
A; Reference number: 158352; MUID:95380169
A; Reference number: 158352; MUID:9780169
A; Reference number: 158352; MUID:978090; PID:91087091
A; Residues: 1-167 < RES>
A; Cross-references: GB:S79251; NID:91087090; PID:91087091
C; Genetics:
A; Genetics:
A; Genetianily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF hc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Cross-references: GDB:579577; OMIM:600431
A.Map postition: 9921-9921
C.Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C.Superfamily: unassigned control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pl6INK4a - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 LILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: GB:S75756; NID:g861470; PIDN:AAD14186.1; PID:g4261886
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAEL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
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    NID:9556197; PIDN:AAA50282.1;
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63.2%; Pred. No. 4.7e-36;
live 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 526; DB 2; L
Pred. No. 3.6e-42;
4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.8%;
Best Local Similarity 82.0%;
Matches 109; Conservative
             A; Cross-references: GB:L36844;
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Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: GDB:CDKN2B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Width - mouse states: Mus sp. (mouse)

Class: Ashmun, R.A.; Hannon, G.J.; Rehberger, P.A.; Trono, D.; Richter, K.H.; W. (mosgene 11, 635-645, 1995)

A; Title: Cloning and characterization of murine pl6INK4a and pl5INK4b genes.

A; Reference number: 188352; MUID:95380169

A; Accession: I78845

A; Accession: I78845

A; Accession: I78845

A; Accession: I78845

A; Cass: Testerences: RES>

A; Molecule type: mRNA

A; Residues: 1-130 <RES>

A; Cross: Testerences: GB:S79252; NID:g1087092; PID:g1087093

C; Genetics:

A; Conso: Testerences: GB:S79252; NID:g1087092; PID:g1087093

C; Genetics:

A; Conso: Testerences: GB:S79252; NID:g1087093

C; Consertion: Musuch and A; Conso: Testerences: GB:S79252; NID:g1087093

C; Consertion: Musuch and A; Conso: Testerences: GB:CF homology; EGF homology; EGF homology; C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
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                                                                                                                                                                                                                                                                                                                                                                                 61 ELLILHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 LATAAARGOVETVRQLLEAGADPNALNRFGRRPIQVMMMGSAQVAELLLLHGAEPNCADP
                                                                                                                                                                         1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA
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             Length 156;
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Pred. No. 1.8e-42;
4; Mismatches 10; Indels
                                                                                             Indels
Score 789; DB 2; L
Pred. No. 1.1e-66;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 1.56
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CDK4 inhibitor p14(INK4B/MTS2) - human
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Best Local Similarity 88.3%;
Matches 106; Conservative
    98.6%;
ilarity 98.7%;
Conservative
                                                Similarity
                                            Best Local Similarity
        Query Match
Best Local 9
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К.Н.

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C;Accession: B57379
R;Hiral, H.; Roussel, M.F.; Kato, J.Y.; Ashmun, R.A.; Sherr, C.J.
Roll: Biol. 15, 2672-2681, 1995
A;Title: Novel INK4 proteins, p19 and p18, are specific inhibitors of the cyclin D-de A;Reference number: A57379; MUID:95257948
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:U20497; NID:9791204; PIDN:AAA85437.1; PID:9791205
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homol
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R;Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
Mol. Cell. Biol. 15, 2682-2688, 1995
A;Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with A;Reference number: A57378; WUID:95257949
A;Reference number: A57378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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A;Residues: 1-168 <HIR>
A;Cross-references: GB:U19596; NID:g790566; PIDN:AAC52193.1; PID:g790567
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C;Keywords: cell cycle control
                                                                                                                                                                                                                                              cyclin-dependent kinase inhibitor p19 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDK4/CDK6 inhibitor p18 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 20-Sep-1999
                       ADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 ADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL-- 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 DRLSGARPRGDVQEVRRLTHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 DWLATAAARGRVEEVRALL-EAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
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40.3%; Pred. No. 1.5e-14;
live 22; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.5%; Score 244; DB 2;
43.7%; Pred. No. 9.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RAAAGGT-----RGSNHARIDAAEGPSDIP 155
                                                                                        -----RAAAGGT-----RGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18; Mismatches
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Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-166 <CHA>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                          C; Accession: A57378
R; Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
R; Chan, F.K.M.; Zhang, J.; Cheng, L.; Shapiro, D.N.; Winoto, A.
A; Title: Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with hom A; Reference number: A57378; MUID:95257949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-16 <4HAA
A; Cross-references: GB:U19597; NID:9790568; PIDN:AAC52194.1; PID:9790569
C; Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C; Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Cross-references: GB:U20498
C.Genetics:
A.Map position: 19p13
C.Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
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                                                                                                                                                                                                                                            cyclin-dependent kinase inhibitor p19 - human
C;Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 22-Jun-1999
                       69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 DRLSGARARGDVQEVRRLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNV 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 258; DB 2;
; Pred. No. 4.8e-17;
17; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31.1%; Score 249; DB 2;
llarity 44.3%; Pred. No. 3.4e-16;
Conservative 18; Mismatches 52;
                                                                                     129 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155
                                                                                                                  120 YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 YLRAAAG----GTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 FLAAESDLHRRDARGLTPLELALQRGAQDLVD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.2%;
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Best Local Similarity 44.18
Matches 67; Conservative
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Best Local Similarity
Matches 70; Conserv
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tus: preliminary
Eccule type: mRNA
A:Residues: 1-164 << HA>
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1 MMMGSAQVAELLLHGAEPNCADPATLTRPVHDAAREGFLD 41

63 PNLKD-GTGFAVIHDAARAGFLDTVQALLEFQADVNIEDNEGNLPLHLAAKEGHLPVVEF 121

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A;Cross-references BMBL Data Library, September 1993
A;Reference number: S37431
A;Accession: S37431
A;Accession: S37431
A;Accession: S37431
A;Accession: S37431
A;Molecule type: mRNA
A;Residues: 1-3924 CCHA>
A;Cross-references: EMBL:226634; NID:9406287; PIDN:CAA81387.1; PID:9406288
A;Cross-references: EMBL:226634; NID:9130466
A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal
A;Recence number: A39643; MUID:91302466
A;Accession: A39643; MUID:91302466
A;Accession: A39643
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2077 COT1>
A;Cross-references: EMBL:256957
A;Accession: B39643
A;Cross-references: EMBL:256958
A;Cross-references: EMBL:3569598
A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.
A;Title: Isolation and A40334; MUID:92009921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Molecule type: DNA
A,Residues: 463-474, PE',477-495 <TSE>
A,Residues: 463-474, PE',477-495 <TSE>
A,Cross references: GB.M37123, NID:g178647; PIDN:AAA62828.1; PID:g178648
B,Chan W.; Kordell, E.; Bennett, V.
J. Cell Biol. 123, 1463-1473, 1393
A,Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and A; Recence number: A49462; MUID:94075409
A,Accession: A49462
A,Status: preliminary; nucleic acid sequence not shown
A,Molecule type: mRNA
A,Residues: 1-3924 <RES>
A,Cross-references: EMBL:226634; NID:g406287; PIDN:CAA81387.1; PID:g406288
                                                                                   ankyrin 2, neuronal long splice form - human N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythro N;Contains: ankyrin L, short form C;Species: Homo sapiens (man) C;Cpate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999 C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569 R;Chan, W.
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A; Cross-references: GDB:127607; OMIM:106410
A; Cross-references: GDB:127607; OMIM:106410
C; Map position: 4q25-4q25-4q25-q292
C; Keywords: alternative splicing
C; ANO2>
C; Keywords: ankyrin repeat homology <ANO2>
C; ANO2>
C; ANO3>
C; 
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F;331-363/Domain: ankyrin repeat
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C.Species: Rattus sp. (rat)
C.Species: Rattus sp. (rat)
C.Species: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 26-May-2000
C.Accession: 152720
R.Knapek, D.F.; Serrano, M.; Beach, D.; Trono, D.; Walker, C.L.
Cancer Res. 55, 1607-1612, 1995
A.Aitile: Association of rat plinkAB/pl6INK4 deletions with monosomy 5 in kidney epithel A.Reference number: 152720; MuID:95228036
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-41 <RES>
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C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
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                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #text_change 20-Sep-1999
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 20-Sep-1999
C;Accession: A55479
R;Gan, K.; Jenkins, C.W.; Li, Y.; Nichols, M.A.; Wu, X.; O'Keefe, C.L.; Matera, A.G., Genes Dev. 8, 2939-2952, 1994
A;Title: Growth suppression by pl8, a p16(INK4/MTS1)- and p14(INK4B/MTS2)-related CDK6
A;Reference number: A55479; MUID:95095079
A;Accession: A55479
                                                                                                                                                                                                                                                                              CDK6 inhibitor p18 - human N;Alternate names: cyclin-dependent kinase N;Alternate names: cyclin-dependent kinase
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A;Map postlino: 1932-1932
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology;
C;Keywords: cell cycle control; protein kinase inhibitor; tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oss-references: GB:U17074; NID:9639713; PIDN:AAC50074.1; PID:9639714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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Best Local Similarity 97.6%; Pred. No. 3.8e-13;
Matches 40; Conservative 1; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.6%; Score 228.5; DB 2
Llarity 40.3%; Pred. No. 2.8e-14;
Conservative 22; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:S77734; NID:g998711
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRAAAGGTRGSNHARIDAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVKHTASNVGHRNHKGDTA 140
                                                  | ::||
| 122 LMKHTACNVGHRNHKGDTA 140
130 LRAAAGGTRGSNHARIDAA 148
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Matches 56; Conserv
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lidues: 1-168 <GUA>
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White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A; Tille: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory
A; Reference number: I49502; MUID:92345717
A; Reference number: I49502
A; Reference number: I495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ankyrin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 149502
                                                                                               PATLIRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL-- 130
                                                                                                                                                                                                                                                                                   571 KNGLT-PLHVAVHHNNLDIVKLLLPRGGS--PHSPAWNGYTPLHIAAKQNQIEVARSLLQ 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            503 LHTAAREGHVDTALALLEKEASQACMTKGFTPLHVAAKYGKVRLAELLLEHDAHPNAAG 562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB: M84756; NID: 9191939; PIDN: AAA37236.1; PID: 9191940
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Pred. No. 0.00013;
7; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. Superfamily: ankyrin; ankyrin repeat homology C. Keywords: alternative splicing
F. 40-72/Domain: ankyrin repeat homology <a href="#">K-40-72/Domain: ankyrin repeat homology <a href="#">K-40-72/Domain: ankyrin repeat homology <a href="#">K-106-138/Domain: ankyrin repeat homology <a href="#">K-139-167/Domain: ankyrin repeat homology <a href="#">K-139-167/Domain: ankyrin repeat homology <a href="#">K-130-1237/Domain: ankyrin repeat homology <a href="#">K-201-233/Domain: ankyrin repeat homology <a href="#">K-207-299/Domain: ankyrin repeat homology <a href="#">K-339-431/Domain: ankyrin repeat homology <a href="#">K-306-398/Domain: ankyrin repeat homology <a href="#">K-308-398/Domain: ankyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <AN15> <AN16> <AN17>
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                                                                                                                                                                                                                                                                                                                                                                                                            131 ---RAAAGGTRGSNHARIDAAEGPSDI 154
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J. Biol. Chem. 268, 9533-9540, 1993
A.fitle: Complex patterns of sequence variation and multiple 5' and 3' ends are found
A.Reference number: S37771; MUID:93252828
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C;Date: 27-May-1994 #sequence_revision 03-Aug-1995 #text_change 13-Aug-1999
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A; Residues: 1-1848 <BIR>
A; Residues: 1-1848 <BIR>
A; Cross-references: EMBLX: K69063; NID:g311816; PIDN:CAA48801.1; PID:g311817
C; Superfamily: ankyrin repeat homology
C; Keywords: alternative splicing
C; Keywords: alternative splicing
F; 48 80/Domain: ankyrin repeat homology <AN01>
F; 81-113/Domain: ankyrin repeat homology <AN02>
F; 114-146/Domain: ankyrin repeat homology <AN03>
F; 114-175/Domain: ankyrin repeat homology <AN04>
F-141-175/Domain: ankyrin repeat homology <AN04>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL--RA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 158; DB 2;
; Pred. No. 3.8e-06;
18; Mismatches 59,
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k; Pred. No. 0.00013;
17; Mismatches 68
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F;562-594/Domain: ankyrin repeat hor F;595-627/Domain: ankyrin repeat hor F;628-660/Domain: ankyrin repeat hor F;61-693/Domain: ankyrin repeat hor F;694-726/Domain: ankyrin repeat hor F;700-792/Domain: ankyrin repeat hor F;700-792/Domain: ankyrin repeat hor F;703-825/Domain: ankyrin repeat hor F;703-825/Domain: ankyrin repeat hor F;703-825/Domain: ankyrin repeat hor
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Best Local Similarity 37.2%;
Matches 48; Conservative 18
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F;275-307/Domain: ankyrin repeat
F;308-340/Domain: ankyrin repeat
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C;Accession:
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C;Date: 27-Jul-1990 #sequence_revision 01-Oct-1992 #text_change 04-Sep-1998
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                                 Naferina to resythrocyte splice form 3 - human
Naferinate names: atyrin 2.1, erythrocyte; ankyrin-R
N;Contains: ankyrin 2.2, erythrocyte
C;Species: Homo sapiens (man)
C;Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 10-Jul-1998
C;Accession: B35049
R;Lambert, S.; Yu, H.; Prchal, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.; Bproc. Natl. Acad Scl. U.S.A. 87, 1730-1734, 1990
A;Tille: CDNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370
A;Status. CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.7%; Score 133.5; DB 2;
35.4%; Pred. No. 0.00032;
tive 15; Mismatches 69;
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Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: GDB:ANK1; ANK
A;Gene: GDB:ANK1; ANK
A;Gene: GDB:118737; OMIM:182900
A; Position: 8p11.2-8p11.2
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A; Molecule type: mRNA
A; Residues: 1-1856 < LAM>
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Matches 52; Conserv
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C;Accession: A35049
R;Lambert, S.; Yu, H.; Profall, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.
R;Lambert, S.; Yu, H.; Profall, J.T.; Lawler, J.; Ruff, P.; Speicher, D.; Cheung, M.C.
R;Let. DNA sequence for human erythrocyte ankyrin.
A;Reference number: A35049; MUID:90175370
A;Accession: A35049
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drosophila drosophila drosophila ceenorhabdi serratia li homo sapien homo sapien mus musculu mus musculu hydra atten homo sapien

P81069 n Q03017 c Q09103 c Q19013 c Q191161 p Q00653 b Q01705 n Q007705 n Q007949 n Q099490 p Q15057 p

GABD\_MOUSE CAT\_DROME KDGE\_DROME GLS1\_CAEEL PHLB\_SERIJ Y148\_HUWAN NTC1\_MOUSE SKD3\_MOUSE SKD3\_MOUSE SKD3\_MOUSE SKD3\_MOUSE SKD3\_MOUSE SKD3\_MOUSE SKD3\_MOUSE SKD3\_MOUSE

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ALIGNMENTS

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Search time 33.95 Seconds (without alignments) 157.404 Million cell updates/sec
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1 MDPAAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156
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GenCore version 4.5 Copyright (c) 1993 · 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_39:\*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000 SUMMARIES

|   |        | Description  | _          | P55271 mus musculu | P42772 homo sapien | ~        | _          | ~          | m          | 3 mus m    | 2 mus m    | homo       | 34 homo    | mus m | 57 homo    | 55 homo    | 5 mus m    | wns          | mus m      | homo       | homo       | rattr    |            | Q06527 chromatium | rattn    |            | homo       | homo       | <pre>07 drosc</pre> | 15         | 12 saccharo | P21783 xenopus lae | 27 homo    | 1982 mus   | Q05921 mus musculu |
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|   |        | ID           | CDN2_HUMAN | CDN5_MOUSE         | CDN5_HUMAN         | CDN5_RAT | CDN2_MOUSE | CDN2_MONDO | CDN7_HUMAN | CDN7_MOUSE | CDN6_MOUSE | CDN6_HUMAN | ANK2_HUMAN | ı     | ANK1_HUMAN | DAPK_HUMAN | NTC4_MOUSE | GABC_MOUSE   | GABB_MOUSE | GABC_HUMAN | GABB_HUMAN | BAR1_RAT | NOTC_BRARE | ANKH_CHRVI        | NTC1_RAT | BAR1_HUMAN | NTC1_HUMAN | ANR3_HUMAN | NOTC_DROME          | BAR1_MOUSE | PH81_YEAST  | NOTC_XENLA         | Y050_HUMAN | NTC3_MOUSE | RNSA_MOUSE         |
|   |        | DB           | ~          | ٦                  | -                  | 7        | -          | -          | -          | ٦          | П          |            | Н          |       | -          | П          | ,          | Н            | Н          | <b>–</b> 1 | ⊣          | П        | н          | Н                 | -        | -          | М          |            | 7                   |            | Т           | Н                  |            | Н          | _                  |
|   |        | Match Length | 156        | 130                | 138                | 130      | 167        | 171        | 166        | 166        | 168        | 168        | 3924       | 1862  | 1880       | 1431       | 1964       | 347          | 382        | 347        | 383        | 768      | 2437       | 323               | 2531     | 777        | 2444       | 832        | 2703                | 765        | 1178        | 2524               | 740        | 2318       | 619                |
| æ | Query  | Match        | 98.6       |                    |                    |          | 57.7       |            | 32.4       | 31.1       | 28.9       | 28.6       | 19.8       | 17.2  | 16.7       | 16.3       | 15.6       | 14.8         | 4          |            | 4          | 14.2     | 14.2       | 4                 | 3        | 3          | 3          | 3          | 3                   | 3.         | ë.          | 'n                 |            | 12.9       |                    |
|   |        | Score        | 789        | 529                | 526                | 524      | 461.5      | 408        | 259        | 249        | 231.5      | 228.5      |            | 3     | 133.5      | m          | 125        | $\leftarrow$ | 118.5      | 117.5      | 117.5      | 114      | 114        |                   | 111.5    | 111        | 110.5      | 109.5      | 107.5               | 107        | $\sim$      | 104.5              | 103.5      | 03         | 103                |
|   | Result | NO.          | н          | 7                  | 3                  | 4        | 2          | 9          | 7          | 80         | 6          | 10         | 11         | 12    | 13         | 14         | 15         | 16           | 17         | 18         | 19         | 20       | 21         | 22                | 23       | 24         | 25         | 26         | 27                  | 28         | 29          | 30                 | 31         | 32         | 33                 |

| RESULT 1D CDN2_HUMAN 1D CDN2_HUMAN 1D CDN2_HUMAN 1D CDN2_HUMAN 1D CDN2_HUMAN 1D CDN2_HUMAN 1D CDN3_HUMAN 1D CDN3_H |
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VARIANTS NON-SMALL CELL LUNG CARCINOMAS (NSCLC).

MEDLINE-94338359; PubMed-8060323;
Hayashi N., Sugimnoto Y., Tsuchiya E., Ogawa M., Nakamura Y.;
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MEDLINE-95375774; PubMed-7647780;
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Pitzgerald M.G., Harkin D.P., Silva-Arrieta S., Macdonald D.J.,
Lucchina L.C., Unsal H., O'Neill E., Koh J., Finkelstein D.M.,
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Medmatot A., Hussain S.P., Hadiwara K., Spillare E.A., Rusin M.R., Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Bennett W.P., Forrester K., Gerwin B., Beach D.H., Harris C.C.; "Mutations in the pillnK4/MTS1/CDKNA, pl51NK4B/MTS2, and pl8 genes primary and metastatic lung cancer.";
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Goldstein A.M., Tucker M.A., Serrano M., Hannon G.J., Beach
Dracopoli N.C.;
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Hum. Mol. Genet. 4:1845-1852(1995).
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ANK 2.
ANK 2.
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ANK 3.
ANK 4.
D -> E (IN A BILIARY TRACT TUMOR).
/FTIG-VARA 001408.
/FTIG-YARA MELIARY TRACT TUMOR AND A FAMILIAL MELANOMA).
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/FIId=VAR_001410.
/FITG=VAR_001411.
G -> D (IN A BILIARY TRACT TUMOR).
/FITG=VAR_001411.
G -> D (IN A PANCREAS TUMOR).
/FITG=VAR_001411.
R -> C (IN MELANOMA).
/FIId=VAR_001413.
                                                                                                                                                                                                                                                                                Moskaluk C.A., Hruban R.H., Lietman A., Smyrk T., Fusaro L., Fusaro R., Lynch J., Yeo C.J., Jackson C.E., Lynch H.T., Kern S.E.; "Novel germline p16INK4 allele (Asp145Cys) in a family with multiple pancreatic carcinomas.";
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PROSITE; PS50297; ANK_REP_REGION; 1.
Cell cycle; Anti-oncogene; Repeat; ANK repeat; Disease mutation; Polymorphism; Li-Fraumeni syndrome; 3D-structure.
REPEAT
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L -> P (IN FAMILIAL MELANOMA).
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                                                                                             Soufir N., Avril M.-F., Chompret A., Demenais F., Bombled J., Spatz A., Stoppa-Lyonnet D., Benard J., Bressac-De Paillerets Hum. Mol. Genet. 7:941-941(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS MELANOMA LEU-48; VAL-57; ASP-89 AND MET-117.
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-!- SIMILARITY: CONTAINS 4 ANK REPEATS.
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                                                                                                                                                                                                                                                      VARIANT PANCREATIC CARCINOMA CYS-146
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EMBL; U12820; AAB60645.1; --
EMBL; U12819; AAB60645.1; JOINED.
EMBL; S69804; AAB60645.1; JOINED.
EMBL; S69804; AAD14048.1; --
EMBL; S69804; --
EMBL;
Genet. 7:209-216(1998).
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REPEAT
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Repeat; ANK repeat.

Cell cycle; Anti-oncogene;

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us-09-016-869a-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quelle D.E., Ashmun R.A., Hannon G.J., Rehberger P.A., Trono D., Richter K.H., Walker C., Beach D., Sherr C.J., Serrano M.; "Cloning and characterization of murine pl6INK4a and pl5INK4b genes."; Oncogene 11:635-645(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNTT: HETERODIMER OF P14 WITH CDK4 (BY SIMILARITY).
-!- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-!- INDUCTION: BY TGF-BETA.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                    ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                      alterations in murine primary T-cell lymphomas.";
Oncogene 14:1361-1370(1997).
-:- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR.
POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
                                                          Gaps
                                                                                 1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                          9
                                                                                                      þγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B).
                       Length 156;
                                                     Indels
121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                      130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHIBITORS.
-!- SIMILARITY: CONTAINS 4 ANK REPEATS.
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PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-95380169; PubMed-7651726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U66085; AAB39833.1; -. EMBL; U66084; AAB39833.1; JOINED.
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:104737; Cdkn2b.
InterPro; IPR002110; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J X DBA;
                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                     RESULT CONS. MOUSE CONS. MOUSE PS5271; OCT-1996
               Query Match
Best Local Simi
Matches 154; (
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-1- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHIBITOR. POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST.
-1- SUBUNIT: HETERODIMER OF P14 WITH CDK4.
-1- DISEASE: CDKN2B MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
-1- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                       "Growth suppression by p18, a p16INK4/MTS1- and p14INK4B/MTS2-related CDK6 inhibitor, correlates with wild-type pRb function."; Genes Dev. 8:2939-2952(1994).
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                         76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell cycle regulator potentially involved in genesis of many tumor pas.":
                                                                                                                                                                            16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                               MEDLINE=95095079; PubMed=8001816;
Guan K.-L., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Keefe C.L.,
Matera G.A., Xiong Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and p18 genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Okamoto A., Hussain S.P., Hagiwara K., Spillare E.A., Rusin M.R., Demetrick D.J., Serrano M., Hannon G.J., Shiseki M., Zariwala M., Xiong Y., Beach D.H., Yokota J., Harris C.C., "Mutations in the pi6INK4/MTSI/CDKN2, p15INK4B/MTS2, and p18 genes primary and metastatic lung cancer."; pcancer Res. 55:1448-1451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-94359613; PubMed-8078588;
Hannon G.J., Beach D.;
"pl5INK4B is a potential effector of TGF-beta-induced cell cycle
                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KIRASE 4 INHIBITOR B (P14-INK4B) (P15-INK4B)
(MULTIPLE TUMOR SUPPRESSOR 2) (MTS2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=94204645; PubMed=8153634;
Kamb A., Gruis N.A., Weaver-Feldhaus J., Liu Q., Harshman K.,
Tavtigian S.V., Stockert E., Day R.S. III, Johnson B.E.,
                                                                                                                       Length 130;
                                                                                                                                                    Indels
                                                                         7AAD60FF552BCFF9 CRC64;
                                                                                                          Score 529; DB 1; L
Pred. No. 2.8e-42;
Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS LUNG ADENOCARCINOMA GLU-47 AND VAL-50.
                                                                                                                                                                                                                                                                                                                                                  138 AA.
                                                                                                                                                   4; Mismatches
                  4 3.5.
                             ANK
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                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
                                                                         13788 MW;
                                                                                                                     66.1%;
88.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 53-138 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 264:436-440(1994).
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 371:257-261(1994).
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                  34
66
100
130
                                                                      130 AA;
                                                                                                                    Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                         38
71
104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDKN2B OR MTS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skolnick M.H.;
                                                                                                                                                                                                                                                                                                                                               CDN5_HUMAN
P42772;
                                                                        SEQUENCE
                            REPEAT
REPEAT
              REPEAT
                                                          REPEAT
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55:1607-1612(1995)
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P51480;
                                                                                                                                                                                                                                                                                                                                                                INIT_MET
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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REPEAT
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                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lisb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                             63 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELG 122
                                                                                                                                                                                                                                                                                                                                                                                                                      65 LLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEERG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 46-86 FROM N.A.
MEDLINE-95228036; PubMed=7712460;
MRDILINE-95228036; PubMed=7712460;
MRDIENE D.F., Serrano M., Beach D., Trono D., Walker C.L.;
"Association of rat pi51N44B/ploinK4 deletions with monosomy 5 in kidney epithelial cell lines but not primary renal tumors.";
                                                                                                                                                                                                                                                                                                                                                                               3 PAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rat
                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR B (P14-INK4B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDITNE-96001392; PubMed-7546221;
MEDITNE-96001392; PubMed-7546221;
Hino O., Kobayashi E., Hirayama Y., Kobayashi T., Kubo Y.,
Tsuchiya H., Kikuchi Y., Mitani H.;
"Molacular genetic basis of renal carcinogenesis in the Eker
"Molacular genetic basis of renal carcinogenesis in the Eker
model of tuberous solerosis (Tsc2).";
Mol. Carcinog. 14:23-27(1995).
                                                                                                                                                                                                                                                                                                                        Score 526; DB 1; Length 138; Pred. No. 5.6e-42;
                                                                                                                                                                                                                                                                                                                                              16; Indels
                                                                                                                                                                                                                                                                                        ODGFFBDFAGFEAD21 CRC64;
                                                                                                                                                                                                                                                       SA -> TP (IN REF. 2).
MISSING (IN REF. 2).
OLL -> HSW (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                         Score 526;
                SIMILARITY: CONTAINS 2 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                         14722 MW;
                                                                                                                       EMBL; U17075; AAC50075.1; -. EMBL; L36844; AAA50282.1; -. EMBL; S69805; AAD14049.1; -.
                                                                                                                                                                                                                                                                                                                        65.8%;
82.0%;
                                                                                                                                                                                                                                                                                                                                                Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norveqicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         HRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                         138 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDKN2B OR INK4.
                                                                                                                                                           MIM; 600431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDN5_RAT
P55272;
                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                          -:- SUBDINIT: HITERODIMER OF P14 WITH CDK4.
-:- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
INITIATION CODONS IN THE SAME READING FRAME.
-:- TISSUE SPECIFICITY: EXPRESSION ABUNDANT IN LUNG, LESS ABUNDANT IN
TESTIS, BARELY DETECTABLE IN LIVER, AND NOT DETECTABLE IN NEONATAL
KIDNEY, ADULT KIDNEY, BRAIN, HEART, OR SPLEEN.
-:- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell cycle; Anti-oncogene; Repeat; ANK repeat; Alternative initiation. CHAIN 130 CYCLIN-DEPENDENT KINASE 4 INHIBITOR B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation and CrCLIN-DEFENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4).
CDKNZA OR, P16INK4A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 ATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENT INHIBITOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVWMMGSARVAELLLLHGAEPNCADP 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
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FOR SHORT ISOFORM.
ANK 1.
ANK 3.
ANK 3.
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Sciurognathi; Muridae; Murinae; Mus
FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. POTENT INHII POTENTIAL EFFECTOR OF TGF-BETA INDUCED CELL CYCLE ARREST (BY
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86.7%; Pred. No. 8e-42;
iive 6; Mismatches 1
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                                                                                                                                                                                                                                                                                INHIBITORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S79760; AAB35360.1; -.
EMBL; S77734; -. NOT_ANNOTATED_CDS.
InterPro; IPR002110; -.
Pfam, PF00023; ank; 3.
PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
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13748 MW;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Matches 104; Conserv
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38
                                                              SIMILARITY).
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                  SO THE THE THE TENT OF THE TEN
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                                                                                                                                                  -!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE INITIATION CODONS IN THE SAME READING FRAME.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMEL; L76150; AAAGOTTO.

MGD; MGI:104738; CdKn2a.

InterPro; IPR002110; -.

Pfan; PF00023; ank; 2.

PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS50297; ANK_REP_REGION; 1.

CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,

CYCLIN-DEPENDENT KINASE 4 INHIBITOR A,

CYCLIN-DEPENDENT.
ogene 11:635-645(1995).
PUGTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS. INHIBITS THE SHOPSHORYLATION OF THE RETINOBLASTOMA PROTEIN BY CDK4 OR CDK6. SUBUNIT: HETEROLIMER WITH CDK4 OR CDK6. PREDOMINANT P16 COMPLEXES CONTAINED CDK6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 4 INHIBITOR A (CDK4I) (P16-INK4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sherburn T.E., Gale J.M., Ley R.D.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6. INHIBITS THEIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monodelphis domestica (Short-tailed grey opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
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63.2%; Pred. No. 6.2e-36;
Live 16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHORT ISOFORM.
FOR SHORT ISOFORM.
ANK 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 129 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155
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                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 2 ANK REPEATS.
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Best Local Similarity 63.23
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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63
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35
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167 AA;
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                                                                                                                                                                                                                         INHIBITORS.
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077617;
  Oncogene
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                                                                                                                        INITIATION CODONS IN THE SAME READING FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; Lr., 2. ank, 3. Pfam; 3. Prosite; PS00023; ank, 3. PROSITE; PS50088; ANK.REPERGION; 1. PROSITE; PS50297; ANK_REP_REGION; 1. Cell cycle; Anti-oncogene; Repeat, Ank repeat; Alternative initiation. 1. 171 CYCLIN-DEPENDENT KINASE 4 INHIBITOR A, 7. ONG TSOORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 CADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 SADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPN 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Bone marrow;
MEDLINE-96121373; PubMed-8575554;
MEDLINE-96121373; PubMed-8575554;
Cokuda T., Hirai H., Valentine V.A., Shurtleff S.A., Kidd V.J.,
Lahti J.M., Sherr C.J., Downing J.R.;
Molecular cloning, expression pattern, and chromosomal localization of human CDKNZD/XINK4d, an inhibitor of cyclin D-dependent kinases.";
Genomics 29:623-630(1995).
ABILITY TO INTERACT WITH CYCLINS D. COULD ACT AS A NEGATIVE REGULATOR OF THE PROLIFERATION OF NORMAL CELLS (BY SIMILARITY).

-!- SUBBNIT: HETERODIMER WITH CDK4 OR CDK6 (BY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: A SHORTER FORM MAY ARISE BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.0%; Score 408; DB 1; Length 171; 69.2%; Pred. No. 5.5e-31; Live 9; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694264F5D0F4F6CC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHORT ISOFORM
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                                                                                                                                                                                                                      SIMILARITY: CONTAINS 3 ANK REPEATS.
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SEQUENCE FROM N.A.
MEDLINE-96362662; PubMed=8741839;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 AA;
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Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                            INHIBITORS.
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SADWLATAAARGRVEEVRALL-EAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEP
                                                                                                                                                                                                                                                                 RESULT 8
CDN7_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Structure of human cyclin-dependent kinase inhibitor p19(INK4d): comparison to known ankyrin-repeat-containing structures and implications for the dysfunction of tumor suppressor p16(INK4a)."; Structure 6:1279-1290(1998). "; FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-: SUMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baumgartner R., Fernandez-Catalan C., Winoto A., Huber R., Engh R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF COMPLEX WITH CDK6. MEDLINE-98421670; PubMed-9751050; Russo A.A., Tong L., Lee J.O., Jeffrey P.D., Pavletich N.P.; Structural basis for inhibition of the cyclin-dependent kinase Cdk6 by the tumour suppressor pl61NK4a.";
                                 Zariwala M., Matera A.G., Xiong Y.; "Isolated inhibitor and characterization of pl9INK4d, a pl6-related inhibitor specific to CDK6 and CDK4":
Mol. Biol. Cell 7:57-70(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; lbuc,
MIM; 600927; -.
MIM; 600927; -.
R interPro; IPR02110; -.
R Pfam; PF00213; ank; 3.
DR PROSITE; P550088; ANK_REP_REGION; 1.
DR PROSITE; P550297; ANK_REP_REGION; 1.
ET REPEAT 41 69 ANK 2.
FT REPEAT 73 102 ANK 2.
TOTAL 106 125 ANK 3.
                                                                                                                                                                                                                                                                                                                                                                   "Mutation testing in melanoma families: INK4A, CDK4 and INK4D.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         Newton Bishop J.A., Harland M., Bennett D.C., Bataille V.,
Goldstein A.M., Tucker M.A., Ponder B.A.J., Cuzick J., Selby P.,
                                                                                                                                                                                    Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; "Identification of human and mouse p19, a novel CDK4 and CDK6 inhibitor with homology to p16ink4."; Mol. Cell. Biol. 15:2682-2688(1995).
          Guan K.L., Jenkins C.W., Li Y., O'Keefe C.L., Noh S., Wu X.,
Zariwala M., Matera A.G., Xiong Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INHIBITORS.
-!- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE-98455510; Pubmed-9782052;
                                                                                                                                                                         MEDLINE-95257949; PubMed-7739548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: U20498; AAA85436.1; -.
EMBL: AF061327; AAC27450.1; -.
PDB; 1BI8; 16-FEB-99.
PDB; 1BDB8; 14-OCT-98.
MIM; 600927; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U49399; AAB1372.1; -. EMBL; U40343; AAB18139.1; -.
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                        TISSUE-Thymus;
                                                                                                                                                                                                                                                                                                                                                       Bishop D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holak T.A.;
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Gaps

9

32.4%; Score 259; DB 1; Length 166; 44.0%; Pred. No. 3e-17; Live 18; Mismatches 60; Indels

66; Conservative

Query, Match Best Local Similarity Matches 66; Conserv

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"Structure 389:999-1003(1997).
-!- FUNCTION: INTERACTS STRONGLY WITH CDK4 AND CDK6.
-!- SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                          71 NCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL 130
                                                                                                                                       Eukaryota; Meiazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=9225748; PubMed=7739547;
MITIAI H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
Hirai H., Roussel M.F., Rato J.-Y., Ashmun R.A., Sherr C.J.;
Novel INTA protebins, pl9 and pl8, are specific inhibitors of the
cyclin D-dependent kinases CDK4 and CDK6.";
Mol. cell. Biol. 15:2672-2681(1995).
Luh F.Y., Archer S.J., Domaille P.J., Smith B.O., Owen D.,
Brotherton D.H., Raine A.R., Xu X., Brizuela L., Brenner S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. OFFICE TO SEQUENCE FROM N.A. Cheng L., Shapiro D.N., Winoto A.; Chan F.K.M., Zhang J., Cheng L., Shapiro D.N., Winoto A.; Indepentification of human and mouse pl9, a novel CDK4 and CDK6 inhibitor with homology to pl6ink4."; Mol. Cell. Biol. 15:2682-2688(1995).
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EWBL; U20497; AAA85437.1; --
PDB; 1AP7; 16-SEP-98.

MGD; MG1:105387; CGKn2d.

InterPro; IPR002110; --
Pfam; PF00023; ank; 3-
PROSITE; PS50089; ANK_REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 1.
Cell cycle; Anti-oncogene; Repeat; 3D-structure.

REPEAT 73 102 ANK 1.

REPEAT 106 135 ANK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            060773; 060794; 166 AA. 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) CYCLIN-DEPENDENT KINASE 4 INHIBITOR D (P19-INK4D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - SIMILARITY: CONTAINS 3 ANK REPEATS.
                                                                                                                                                                                                                                                131 RAAAG----GTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                   127 AAESDLHRRDARGLTPLELALQRGAQDLVD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRUCTURE BY NMR. MEDLINE-98013176; PubMed-9353127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=C57BL KAPLAN;
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CDN6_HUMAN
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MEDLINE-55257948; Pubmed=7739547;
MEDLINE-55257948; Pubmed=7739547;
MITAL H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
Hiral H., Roussel M.F., Kato J.-Y., Ashmun R.A., Sherr C.J.;
HIRAL PROCLEIDS, p19 and p18, are specific inhibitors of the cyclin D-dependent kinases CDK4 and CDK6.";
MOL. Cell. Biol. 15:2672-2681(1995).
-1- FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INHIBITS CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDOGRNOUS RETINOBLASTOMA PROTEIN RB.
-1- SUBJUNT: HETERODIMEN OF P18 WITH CDK6 (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE CDKNZ FAMILY OF CYCLIN-DEPENDENT KINASE
                                                                                                                                                               73 ADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYL-- 130
                                                                                                                                                                             10 DRLSGARARGDVQEVRRLHRELVHPDALNRFGKTALQVWMFGSPAVALELLKQGASPNV 69
                                                                                                              DWLATAAARGRVEEVRALL-EAVALPNAPNSYGRRPIQVMMGSARVAELLLLHGAEPNC 72
                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT
                                                                                      18;
                                                               Length 166;
                                                            31.1%; Score 249; DB 1; Length 16
44.3%; Pred. No. 2.5e-16;
ive 18; Mismatches 52; Indels
ANK 3.
A -> P (IN REF. 2).
9E74F5C23B7EBCB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC88D5489307E128 CRC64;
                                                                                                                                                                                                                                129 ESDLHHRDASGLTPLELARQRGAQNL-MDILQGHMMIP 165
                                                                                                                                                                                                                131 -----RAAAGGT-----RGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                       168 AA
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PROSITE; PS50088; ANK_REPEAT; 2.
PROSITE; PS50297; ANK_REP_REGION; 1.
Cell cycle; Repeat; ANK_repeat.
REPEAT 4
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ANK 2.
ANK 3.
ANK 4.
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98
132
AN
165
AN
18066 MW;
166 AN
17
17894 MW;
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                                                                                      Conservative
                                                                                                                                                                                                                                                                                                     STANDARD;
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InterPro; IPR002110;
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102
136
168 AA;
                         166 AA;
                                                              Query Match
Best Local Similarity
Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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Q60772;
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SEQUENCE
REPEAT
CONFLICT
SEQUENCE
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CDN6_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDILINE-98100086; PubMed-9437433; Venkataramani R., Swaminathan K., Marmorstein R.; Venkataramani R., Swaminathan K., Marmorstein R.; Structure of the CDK4/6 inhibitory protein pl81NK4c provides insights into ankyrin-like repeat structure/function and tunor-derived pl61NK4 mutations."; Nat. Struct. Biol. 5:74-81(1998).
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                                                                                                                                                                                                                                                                                70 PNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARY 129
                                                           Gaps
                                                                                                                  10 EPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAE 69
                                                                                                                                                      Li J., Byeon I.-J.L., Ericson K., Poi M.-J., O'Maille P., Selby T., Tsai M.-D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blais A., Labrie Y., Pouliot F., Lachance Y., Labrie C.; "Structure of the gene encoding the human cyclin-dependent kinase inhibitor p18 and mutational analysis in breast cancer."; Blochem. Blophys. Res. Commun. 247:146-153(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CYCLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95095079; PubMed-8001816; Guan K., Jenkins C.W., Li Y., Nichols M.A., Wu X., O'Reefe C.L., Matera G.A., Xiong Y.;
                                                           1;
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"A pl8 mutant defective in CDK6 binding in human breast cancer cells.";
Length 168;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND VARIANT BREAST CANCER PRO-72. TISSUE=Breast;
                                                           (09
   DB 1;
Ouery Match 28.9%; Score 231.5; DB Best Local Similarity 40.3%; Pred. No. 1e-14; Matches 56; Conservative 22; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
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MEDLINE=96438606; Pubmed=8840966;
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                                                                                                                                                                                                                                                                                                                                                                                                                122 LMKHTACNVGHRNHKGDTA 140
                                                                                                                                                                                                                                                                                                                                                                  130 LRAAAGGTRGSNHARIDAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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STRUCTURE BY NMR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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P42773;
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TAME TO THE TOTAL 
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                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CDKN2 FAMILY OF CYCLIN-DEPENDENT KINASE
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                                                                                                                                 ALSO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
FUNCTION: INTERACTS STRONGLY WITH CDK6, WEAKLY WITH CDK4. INH. CELL GROWTH AND PROLIFERATION WITH A CORRELATED DEPENDENCE ON ENDOGENOUS RETINOBLASTOMA PROTEIN RB.
                                                                                                                       TISSUE SPECIFICITY: HIGHEST LEVELS FOUND IN SKELETAL MUSCLE. FOUND IN PANCREAS AND HEART.
DISEASE: CDKN2C MUTATIONS ARE INVOLVED IN TUMOR FORMATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIN; vor.
InterPro; IPR002110,
Pfam; PF00023; ank; 3.
Pfam; PF00023; ank; 3.
PROSITE; PS50088; ANK_REPERGION; 1.
PROSITE; PS600297; ANK_REPERGION; 1.
REPEAT 33 ANK 1.
REPEAT 7 A ANK 2.
REPEAT 7 ANK 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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001484; 001485;
01-AR-1993 (Rel. 25, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FTIG=VAR_001490.
5D66AFA715186E9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28.6%; Score 228.5; DB 1;
40.3%; Pred. No. 2e-14;
tive 22; Mismatches 60;
                                                                                                       SUBUNIT: HETERODIMER OF P18 WITH CDK6.
                                                                                                                                                                                                                                                                   INHIBITORS.
-:- SIMILARITY: CONTAINS 4 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U17074; AAC50074.1; -
EMBL; AF0412348; AAC39783.1; -
EMBL; AF041250; AAC39783.1; -
EMBL; AF041249; AAC39783.1; JOINED.
PDB; IIHB; 13-JAN-99;
PDB; IBU9; 13-SEP-99.
MIN; 603369; -
Interpro; IPR002110; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1)
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 AA; 18127 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 LRAAAGGTRGSNHARIDAA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVKHTASNVGHRNHKGDTA 140
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nes 56; Conservative
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ANK2_HUMAN
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Matches
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REDIESGE-Brain and Selective localization in unspecified according to the major developmentally regulated 4.40.6 may read may receive to claim the major development of the major developm
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     regulatory domain.";
Mamm. Genome 3:281-285(1992).
-!- FUNCTION: ATTACL INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS: BIND TO THE ETHYROCYTE MEMBRANE PROTEIN BAND 4.2, TO
NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     International In
                                                                                                                                                                                                                            EXTURNOLITE ANX PRINCE ANY PROPERTY (BETA CHAIN) TO DESMIN EXTURNOLITE ANX PROPERTY (BETA CHAIN) TO THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; THEY RETAIN MOST OR ALL OF THESE BINNING FUNCTIONS.

-!- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC PLASMA MEMBRANE.
-!- PTM: REGULARTED BY PHOSPHORYLATION (BY SIMILARITY).
-!- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
-!- PTM: ACYLATED SA PALMITIC ACID GROUP(S) (BY SIMILARITY).
                                          Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Musinae; Mus.
                                                                                                    TISSUE=Erythrocyte;

BDLINE-92345717: PubMed=1386265;
White RA., Birkenmeler C.S., Peters L.L., Barker J.E., Lux S.E.,
"Murine erythrocyte ankyrin cDNA: highly conserved regions of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN).
55 KDA REGULATORY DOMAIN (REGULATES
THE BINDING OF ANKYRIN TO SPECTRIN
AND THE BAND 3 PROTEIN).
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                                         Chordata; Rodentia;
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HSSP; Q00420; 1AWC.
MGD; MGI:88024; Ankl.
InterPro; IPR000968; -.
InterPro; IPR00310; -.
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1102
1135
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1197
1230
2263
329
3329
4428
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4428
626
626
                               Mus musculus (Mouse)
                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                        SEQUENCE FROM N.A.
                                                                   NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
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MISSING (IN ISOFORM 2 AND ISOFORM 3).
GQ -> PE (IN REF. 4).
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-> HA (IN REF. 2).
-> Y (IN REF. 2).
52AC496C428E29D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  (APPROXIMATE)
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                                                                                                                                                                                                                                                                            REPEAT-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.8%; Score 158; DB 1; 37.2%; Pred. No. 2.1e-06; iive 18; Mismatches 59
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ID ANK1_MOUSE

AC 002357;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-OCT-2000 (Rel. 40, Last annotation update)
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Best Local Similarity
Matches 48; Conserv;
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587 AAADSAGKN 595
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VARSPLIC
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SEQUENCE
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MEDLINE-952256'."

MEDLINE-952256'."

MEDLINE-952256'."

MEDLINE-952256'.

MEDLINE-952256'.

MEDLINE-952256'.

MANYUN. GONZALEZ J., Kugler W., Oezena R., Pekkun A.,

Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;

Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;

Mutations are a major cause of dominant and recessive

Thereditary spherocytosis ";

Mar, Genet. 13:214-218 [1996].

Herditary spherocytesis ";

Nat. Genet. 13:214-218 [1996].

"I. PERMITS BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO

NA-K APPASE, TO THE EXPHROCYTE MEMBRANE PROTEIN BAND 4.2, TO

NA-K APPASE, TO THE EXPHROCYTE MEMBRANE PROTEIN BAND 4.2, TO

NA-K APPASE, TO THE EXPHROCYTE MEMBRANE PROTEIN BAND TO THE

CYTOSKELETAL PROTEINS FOREIN, TUBULIN, VIMENTIN AND DESMIN.

CYTOSKELETAL PROTEINS FOREIN, TUBULIN, VIMENTIN AND DESMIN.

CYTOSKELETAL DOMAIN OF THE EXPTHROCYTES ANDON EXCHANGE PROTEIN;

C'TOSKELLOLAR LOCATION: CYTOPLASMIC SURRACE OF ERYTHROCYTIC

PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                       Lux S.E., John K.M., Bennett V.; "Analysis of DONA for human erythrocyte ankyrin indicates a repeated structure with homology to tissue-differentiation and cell-cycle control proteins.";
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                  16 LATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQV-MMMGSARVAELLLLHGAEPNCAD 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2).
                                                                                                                                                                                                                                                                                                                                                                        75 PATLTRPVHDAAREGFLDTL-VVLHRAGARLDVRDAW-GRLPVDLAEELGHRDVARYL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲,
                                                                                                                                                                                                                           11;
                                                                                                                                                                              17.2%; Score 137.5; DB 1; Length 1862; 34.7%; Pred. No. 7.3e-05;
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                                                                                                                                                                                                                           Indels
                                                                                                                     AE6B85B5B29001E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS
                                                                                                                                                                                                                           68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90175370; PubMed-1689849;
Lambert S., Yu H., Prchal J.T., Lawler J., Ruff
Cheung M.C., Kan Y.W., Palek J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "cDNA sequence for human erythrocyte ankyrin.";
Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990)
                                                                                                                                                                                                                           17; Mismatches
                                                         ANK 22.
ANK 23.
DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       620 YGGSANAESVQGVTPLHLAAQEGHTEM 646
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21
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MEDLINE-90158830; PubMed-2137557;
  ANK
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01-APR-1990 (Rel. 14, Last sequ
01-OCT-2000 (Rel. 40, Last anno
                                                                                                                       204242
                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 344:36-42(1990).
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                                                                                                                                                                                                      Best Local Similarity
Matches 51; Conserv
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P16157;
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SEQUENCE
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1 -> D (IN ISOFORM 2.2).

TVEGLEDSELEVOIDYFWKHSKDHTSTRNP -> ELRGS
GLQPDLIEGRKGAQIVKRASLKRGKQ (IN A THIRD
VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY THE SEQUENCE SHOWN IS THAT OF ANKYRIN
                                                                                                     PTM: ACYLATED BY PALMITIC ACID GROUP(S).
DISEASE: DEFECTS IN ANKI ARE THE CAUSE OF DOMINANT AND RECESSIVE HEREDITARY SPHEROCYTOSIS (HS).
SIMILARITY: CONTAINS 23 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KDA DOMAIN (ANION EXCHANGE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; PF00531; death; 1. PR0531E PF00531; death; 1. PR051TE; PS50088; ANK REPEAT; 20. PR051TE; PS50017; DEATH_DOMAIN; 1. PR051TE; PS50017; DEATH_DOMAIN; 1. PR051TE; PS50017; DEATH_DOMAIN; 1. Phosphorylation; Lipopcrotein; Multigene family; Disease mutation; Elliptocytosis; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN).
55 KDA REGULATORY DOMAIN (REGULATES
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BINDING DOMAIN)
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                                                                                       PTM: REGULATED BY PHOSPHORYLATION. PTM: ACYLATED BY PALMITIC ACID GRO
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           ALTERNATIVE PRODUCTS:
ALTERNATIVE SPLICING.
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Pfam; PF00023; ank; 22.
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PIR; A35049; A35049.
HSSP; Q00420; IAWC.
MIM; 182900; -
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us-09-016-869a-2.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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W; 9EE84811004A155B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 130.5; DB 1;
Pred. No. 0.00024;
1; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
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ATP (BY SIMILARITY).
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ANK 8.
ANK 9.
ANK 10.
                                                                                                                                                                               PROSITE; PS50297; ANK_REPERT; 6.
PROSITE; PS50297; ANK_REP_REGION; 1.
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NTG4_MOUSE STANK...
P31695, Q62389;
01-JUL-1993 (Rel. 26, Created)
". MOV-1997 (Rel. 35, Last seque
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                                                                        EMBL; X76104; CAA53712.1; -. HSSP; Q63450; 1A06.
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InterPro; IPR000719; -.
InterPro; IPR002210; -.
InterPro; IPR002290; -.
Pfam; PF00023; ank; 8.
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SEQUENCE FROM N.A.
MEDLINE-95129831; PubMed=7828849;
Deiss L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
Diess L.P., Feinstein E., Berissi H., Cohen O., Kimchi A.;
"Identification of a novel serine/threonine kinase and a novel 15-kr
protein as potential mediators of the gamma interferon-induced cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
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-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: CONTAINS 10 ANK REPEATS.
-!- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                 Length 1880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (DAP KINASE 1).
                                                                                                                                                                                                                                                                      Indels
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-> I (IN REF. 2).
1C5F5E7EFD1CD428 CRC64;
                                                                                                                                   /FTId=VAR_000601.
D -> N (IN DUESSELBORF).
                           /FTId=VAR_000596.
R -> H (IN BRUEGGEN).
                                                                                                                                                                                                                                                                      :69
                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                             Score 133.5; DB 7
Pred. No. 0.00017;
      /FTId=VAR_000595.
V -> I (IN HS).
                                                                                                                                                        /FTId=VAR_000602.
R -> D.
                                       .. LIN BRUEGG /FTId=VAR_000597.
                                                                                                      /FTId=VAR_000600.
E -> D
                                                                                                                                                                      R -> D.
/FTId=VAR_000603.
                                                                       /FTId-VAR_000598
                                                                                           /FTIG=VAR_000599
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1880 AA;
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P53355;
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PROSITE; PS50297; ANK_KEL_LAGGET, PROSITE; PS5017; DEATH_DOMAIN; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
PROSITE; PS50010; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; Calmodulin-binding; Phosphorylation; ATP-binding; Repeat; ANK repeat; Apoptosis.
Phosphorylation; ATP-binding; Repeat; ANK R
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update)
01-0CT-2000 (Rel. 40, Last annotation update)
NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3).
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EGF-LIKE 1.
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EGF-LIKE 4.
EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6.
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SIGNAL 1 20 POTEWILAL.
CHAIN 21 1964 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4.
DOMAIN 21 1443 EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                 Unytendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;
"Notch4/int-3, a mammary proto-oncogene, is an endothelial
cell-specific mammalian Notch gene.";
ell-specific mammalian Notch gene.";
-: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-: DISEASE: ACTIVARED INT-3 TRANSPORMS MAMMARY EPITHELIAL CELLS.
-: SIMILARITY: CONTAINS 29 EGF-LIKE DOMAINS.
-: SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                               REVISIONS, SEQUENCE FROM N.A.
MEDLINE=97294599; PubMed=9150355;
Gallahan D., Callahan R.;
"The mouse mammary tumor associated gene INT3 is a unique member of the NOYCH gene family (NOYCH4).";
Oncogene 14:1883-1890(1997).
                                           SEQUENCE FROM N.A.
MEDLINE-92194507; PubMed-1312643;
Robbins J., Blondel B.J., Gallahan D., Callahan R.;
Robbins Li Brondel B.J., Gallahan D., Callahan R.;
"Mouse mammary tumor gene int-3: a member of the notch gene family transforms mammary epithelial cells.";
J. Virol. 66:2594-2599(1992).
      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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InterPro: IPR001438; -.
InterPro: IPR00181; -.
Pfam: PF00008; EGF: 27.
Pfam: PF00006; motch: 2.
PRNWS: PR00006; motch: 2.
PRNWS: PR00006; motch: 2.
PRNWS: PR00010; ASK_REPEAT: 5.
PROSITE: PS00209; ANK_REPERGION; 1.
PROSITE: PS00010; ASK_HYDROXYL; 11.
PROSITE: PS00118; EGF_1; 28.
PROSITE: PS01187; EGF_2; 21.
PROSITE: PS01187; EGF_2; 31.
PROSITE: PS01187; EGF_CA; 9.
Differentiation: Neurogenesis: Nepeat;
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TISSUE-Lung, and Testis;
MEDLINE-96281668; PubMed-8681805;
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HSSP; P00740; 1IXA.
MGD; MGI:107471; Notch4.
InterPro; IPR000152; -.
InterPro; IPR000561; -.
InterPro; IPR000800; -.
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1964
                     4CBI_TaxID=10090;
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Search completed: October 31, 2001, 07:11:36 Job time: 473 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

October 31, 2001, 07:04:48; Search time 117.56 Seconds (Without alignments) 175.566 Million cell updates/sec

US-09-016-869A-2

800 1 MDPAAGSSMEPSADWLATAA.....TRGSNHARIDAAEGPSDIPD 156 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

425026 l number of hits satisfying chosen parameters:

425026 seqs, 132305027 residues

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Database :

sp\_plant:\*
sp\_rodent:\*
sp\_rodent:\*
sp\_unclassified:\*
sp\_vertebrate:\*
sp\_virus:\* SPTREMBL\_16:\*

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2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\* sp\_organelle:\* sp\_phage:\* sp\_mhc:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

|   | Description              | Ognot Flores | Oged33 mesocricetu | Ogros mesocricetu | P97510 mis misculu | 080088 mis miscuin | Odve51 felie eilus | Obtant our conofe | Obesto folia ailio | Comfo certs Silve | Obelot min america | Operation mus spreams | nTnosmus muscaTa | OFABA SUS SCIOIS | Sing   | 2 2    | 000    | and a  | Spin S | Spill  | Obdwn4 mus musculu |
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| ф | Query<br>Match           | 68.5         | 63.8               | 59.6              | 59.5               | 59.2               | 56.1               | 55.5              | 53.4               | 51.1              | 51.0               | 51.0                  | 50.9             | 50.6             | 41.8   | 41.4   | 40.9   | 40.8   | 40.8   | 30.3   |                    |
|   | Score                    | 548          | 510                | 476.5             | 476                | 474                | 449                | 444               | 427                | 409               | 408                | 408                   | 407              | 405              | 334    | 331    | 327    | 326    | 326    | 314 5  | 1                  |
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| 2 124<br>124<br>125<br>127<br>127<br>128<br>138<br>138<br>138<br>138<br>138<br>138<br>138<br>13                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                         |
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## ALIGNMENTS

Pred. No. 7e-34;

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EPNCEDPATLSRPVHDAAREGFLETLAILHQAGARLDVLDARGRLPVDLALERGHCDVVQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
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                                                                                                                                           Mesocricetus auratus (Golden hamster).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Muscarella P., Knobloch T.J., Weghorst C.M.; Knobloch T.J., Weghorst C.M.; Knobloch Syrian Golden Hamster CDKN2/MTS1 Gene and "Sequencing of the Syrian Golden Hamster CDKN2/MTS1 Gene and Identification of Inactivating Alterations in Hamster Tumor Cell
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STRAIN-F344/N; TISSUE-LUNG;
STRAIN-F344/N; TISSUE-LUNG;
SWEDLINE-9718461; PubMed-9032263;
SWafford D.S., Middleton S.K., Palmisano W.A., Nikula K.J.,
Tesfâlgzi J., Baylin S.B., Herman J.G., Bellinsky S.A.;
"Frequent aberrant methylation of pl6INK4a in primary rat lung
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SEQUENCE 159 AA; 17366 MW; 3C4CA920AlfEAEB6 CRC64;
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                                                                   01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
11-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                            63.8%; Score 510; DB 11; 68.9%; Pred. No. 8.9e-37;
                                      157 AA
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121 YLRAAGNTPQGSEPAGVTSAQTPPEVSD 148
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAY-2001 (TrEMBLrel. 16, Last anno
1916 PROTEIN P16.HK4A.
Rattus norvegicus (Rat).
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PROSITE; PS50297; ANK_REP_REGION; 1.
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EMBL; L81167; AAD48924.1; -.
HSSP; Q60773; 1AP7.
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence variation and chromosomal mapping of the murine Cdkn2a tumor
                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLRel. 16, Last annotation update)
02-CELIN DEPENDENT KINASE INHIBITOR PLOFINKAA (PLÉINKAA TUMOR SUPPRESSOR
PROTEIN) (CYCLIN DEPENDENT KINASE INHIBITOR PROTEIN).
DEPENDENT KINASE INHIBITOR PROTEIN).
CENKUNA OR EJALPHA OR PLÉINKAA.
                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-DBA/ZN; TISSUE-SPLEEN;
MEDLINE-98151529; PubMed-9482902;
Zhang S., Ramsay E.S., Mock B.A.;
"Cdkn2a, the cyclin-dependent kinase inhibitor encoding p16INK4a and p19ARF, is a candidate for the plasmacytoma susceptibility locus, Pctrl.";
                                                                                                            EPNCADPATLIRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
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MEDILNE-9128829;
SOLOff E.V., Herzog C.R., You M.;
"The 5'-flanking region of the El alpha form of the murine pl6INK4a
                                    MEPSADWI,ATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Malumbres M., de Castro I., Santos J., Melendez B., Mangues Serrano M., Pellicer A., Fernandez-Piqueras J.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gressani K.M., Rollins L.A., Miller M.S.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998)
                                                                                                                                                                                                                                                                                                                     168 AA.
 11; Mismatches
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=DBA/2, AND C57BL/6;
MEDLINE=95380169; Pubmed=7651726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=VARIOUS STRAINS;
MEDLINE=97179476; PubMed=9021155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-42 FROM N.A. STRAIN-DBA/2, AND C57BL/6; Gressani K.M., Rollins L.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1-155 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       suppressor gene.";
Mamm. Genome 8:65-66(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-11 FROM N.A.
     97; Conservative
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6J X DBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herzog C.R., You M.;
                                                                                                                                                                                                                            121 YLRYLLSSAG 130
                                                                                                                                                                                         129 YLR---AAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                      P97510; P97937
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TISSUE-PBNC;
Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y.,
Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M.,
Nishigaki K., Watari T., Tsujimoto H., Hasogawa A.;
"Cloning and chromosomal mapping of the felline genes p16(MTS1/CDKN2A),
and p15(WTS2/CDKN2B).";
Submitted (JAN-1998) ",
EMBL, AB010807; BAA33540.1; -.
HSSP; P4271, 1B17.
InterPro; IPR002116; -.
Pfam; PF00023; ank; 3.
                   murine Cdkn2a tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-42 FROM N.A. STRAIN-BALB/CJ AND MUS MUS POSCHIAVINUS;
Santos J., Malendez B., Perez de Castro I., Malumbres M., Serrano M.,
Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HESAADRIARAAAGGRVPDVRALLEAGVSPNAPNSFGRTPIQVMMGNVHIAALLLNYGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 168;
                                                                                                                                                                                                                        in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; AF044335; AAC08062.1;
EMBL; U49279; AAC00051.1;
EMBL; U79626; AAD00224.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356A973BEAC4D167 CRC'64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10824 MW; 26399FF21359F35D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
Herzog C.R., You M.; Saquence variation and chromosomal mapping of the suppressor gene."; Mamm. Genome 8:65-66(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 59.2%; Score 474; DB 11; Best Local Similarity 63.2%; Pred. No. 1.2e-33; Matches 98; Conservative 17; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.1%; Score 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50297; ANK_REP_REGION; 1.
SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 AA; 17915 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P16/CDKN2A/MTS1 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                           HSSP; P55273; 1BD8.
MGD; MGI:104738; Cdkn2a.
InterPro; IPR002110; -.
Pfam; PF00023; ank; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinase;
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01-NOV-1998 (TIEMBLIEL. 08, Last sequence update)
01-NAR-2001 (TIEMBLIEL. 16, Last annotation update)
CYCLIN DEPENDENT KINASE INHIBITOR P16INK4A (P16INK4A TUMOR SUPPRESSOR ENGYEIN) (CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN).
                                                                                  STRAIN=CAST/E1, C57BL/6J, ARF/J, AND MOLF/E1;
Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M.,
Pellicar Analysis of the pl6(INK4a) and pl5(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; J49280; AAC08963.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 EPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVAR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BALB/CRNPT: TISSUE-SPLEEN;
MEDLINE-98151529; PubMed-9482902;
Zhang S., Ramsay E.S., Mock B.A.;
"CdknZa, the cyclin-dependent kinase inhibitor encoding pl6INK4a and P19ARF, is a candidate for the plasmacytoma susceptibility locus, Pctrl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 MEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVAELLLLHGA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 AA; 17941 MW; 9A6B0F24F34D5FEC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 95:2429-2434(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 476; DB 11;
; Pred. No. 8.2e-34;
16; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 YLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 YLRSAGCSLCSAGWSLCTAGNVAQTDGHSFSSSTP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00023; ank; 4.
PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=MA/M4J;
MEDLINE=97179476; PubMed=9021155;
                                                                                                                                                                                                                                                 U49280; AAC00052.1; --
U66087; AAB39600.1; --
U66086; AAB39600.1; JOINED.
AF004588; AAB61416.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                           ; U47018; AAC52987.1; -. U79628; AAD00226.1; -. U79625; AAD00223.1; -. U79625; AAD00225.1; -. P42771; 1B17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59.5%;
63.9%;
                                                                 SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-42 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 59.59
Best Local Similarity 63.99
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:104738; Cdkn2a.
rPro; IPR002110; -.
(MTS1) gene.";
Gene 180:213-215(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00248; ANK; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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SEQUENCE
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Length 102;

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Indels

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RESULT Q9TSY1

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51 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 110
Okuda M., Cho K., Setoguchi A., Minehata K., Yazawa M., Endo Y., Nishigaki K., Watari T., Tsujimoto H., Hasegawa A.; "Cloning and chromosomal mapping of the feline genes p16(MTS1/CDKNZA) and p15(MTS2/CDKNZB)."; the EMBL/GenBank/DDBJ databases. EMBL; AB010808; BAA33541.1; -. HSSP; P5527; BBB. InterPro; IPR002110; -. Pfam; PF00023; ank: 2. PROSTE; P55023; ank: 2. PROSTE; P550297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                        51 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 81;
                                                                                                                                                                                                                                                        Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Venkatraj V.S., Mayor J., Modiano J.F.;
Venkatraj V.S., Mayor J., Modiano J.F.;
"Role of pl6/Ink4-a in familial canine cancers.";
Submitted (FBB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF234176; AAG01087.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAX-1999 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 AA; 8868 MW; 0E39D8D805BEACOF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                      86 AA; 9340 MW; A59FF0193290E867 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE 4/6 INHIBITOR-A (FRAGMENT).
                                                                                                                                                                                                                                                      53.4%; Score 427; DB 6;
97.6%; Pred. No. 6.3e-30;
live 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  111 GRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                     61 GRLPVDLAEERGHRDVARYLRAAAG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GRLPVDLAEELGHRDVARYL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GRLPVDLAEELGHRDVARYL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.8
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                             83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canis familiaris (Dog)
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9615;
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NON_TER
SEQUENCE
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SEQUENCE
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Q921C1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Q9GMF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                  Gaps
                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
15/WTS2/CDKNZB (FRAGNENT).
Felis silvestris catus (Cat.).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                  .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEGUENCE FROM N.A.
STRAIN-LARGE WHITE;
Le Chalony C., Hayes H., Frelat G., Geffrotin C.;
"Identification and mapping of swine CDKN2A and CDKN2B exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AJ242787; CAB65454.1; -...
HSSP; P42771; IBT7.
InterPro; IPR0001398; -...
InterPro; IPR002110; -...
Pfam; PF00023; ank; 2...
ProDom; PD001180; -.; 1...
PROSITE; PS650297; ANK_REP_REGION; 1.
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5D23ABCC1088DE0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR, P16 (FRAGMENT)
                                  11;
                                                                                                                                                            111 GRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEG 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 444; DB 6;
Pred. No. 2.7e-31;
5; Mismatches 11;
                    Pred. No. 9.8e-32;
                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 AA; 11023 MW;
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84.3%;
                    86.08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                        Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103
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Best Local Similarity
tches 86; Conserv
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                  Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
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SEQUENCE
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Euteleostomi; Canis.

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Gaps

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09XS52;

09XS52 æ

RESULT Q9XS52

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1 VMMMGSAQVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVCDAW 60
                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
STRAIN=LARGE WHITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kinase; Cyclin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                          Q9TSY0
Q9TSY0;
                                                                                                                                                                                                                                                                                                                                                                               CDKN2B.
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                                                                                                                                                                              RESULT 12
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                                                                                                                                                               Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;

"Comparative analyzis of the p16(INK4a) and p15(INK4b) DNA sequences submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; U79637; AD00237.1; -.

HSSP; P55273; 1BD8.

InterPro; IPR002110; -.

PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Pellicer A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79639; AAD00234.1;
EMBL; U79636; AAD00233.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 408; DB 11; Length 86;
Pred. No. 2.7e-28;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.0%; Score 408; DB 11; Length 86; 92.9%; Pred. No. 2.7e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2011 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509D9B3613251B18 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 GRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spretus (Western wild mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.0%;
92.9%;
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9269 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best_Local Similarity 92.9
Matches 79; Conservative
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86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86 AA;
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les 79; Conserv
                                                                                                 [1]
SEQUENCE FROM N.A.
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                                                                       NCBI_TaxID=10096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                               STRAIN-SPRET/EI;
                                                                                                                                                                                                                                                                                                                                                                                                                                               86
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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Matches
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1D Q9
DDT Q99
DDT Q11
DDT Q11
DDT Q1
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51 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 110
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                       Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                    Le Chalony C., Hayes H., Frelat G., Geffrotin C.; "Identification and mapping of swine CDKN2A and CDKN2B exon2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 407; DB 6; Length 86;
Pred. No. 3.3e-28;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malumbres M., Pellicer A.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF015460; AAB94534.1; -.
HSSP; P55273; IBD8.
InterPro; IPR002110; -.
PROSITE; PS50297; ANK FEP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TFEMBLrel. 06, Last sequence update)
01-MAR-2001 (TFEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR PISINK4B (FRAGMENT).
                                                                                                                                                                                                                                                       Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16EF7A223293CCF9 CRC64;
                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CYCLIN-DEPENDENT KINASE INHIBITOR P15 (FRACMENT).
                                                                                                                                  86 AA.
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PROSITE; PS50297; ANK_REP_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
111 GRLPVDLAEELGHRDVARYLRAAAG 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 AA; 9286 MW;
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HSSP; P55273; 1BD8.
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Best Local Similarity 92.99
Matches 79; Conservative
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Query Match
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                                                                                     51 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Santos J., Melendez B., Perez de Castro I., Malumbres M., Serrano M., Perlandez-Piqueras J.;
Pellider A., Fernandez-Piqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U79634; AAD00236.1; --
EMSSP; P55273; 1808.
                                                             Gaps
                                                                                                  1 VMAMGNVHVAALLLNYGADSNCEDPTTFSRPVHDAAREGFLDTLVVLHGSGARLDVRDAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                 Mus spretus (Western wild mouse).
Bukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10096;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GRLPVDLAEELGHRDVARYLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                                                             Indels
                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 113 113
113 AA; 12073 MW; C3BFE8325DB2D79E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 13, Last sequence update) CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT).
0499DB26144FB6DF CRC64;
                                                                                                                                                                                                                                                                                         CYCLIN-DEPENDENT KINASE INHIBITOR PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.8%; Score 334; DB 11;
61.1%; Pred. No. 9.1e-22;
                                   11;
                                    Score 405; DB 11
Pred. No. 5e-28;
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                                                             4; Mismatches
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                                                                                                                                       111 GRLPVDLAEELGHRDVARYLRAAAG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00023; ank; 2.
PROSITE; PS50297; ANK_REP_REGION;
                                                                                                                                                    61 GRLPVDLAEEQGHRDIARYLHAASG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                    Ouery Match 50.6%;
Best Local Similarity 91.8%;
Matches 78; Conservative
                                                                                                                                                                                                                                         Q921C2;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2001 (TrEMBLrel. 16,
 9237 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002110; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00248; ANK;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
 AA;
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRET/EI;
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 86
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SEQUENCE
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Q9QWH5
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STRAIN-MUS MUSCULUS;
STRAIN-MUS MUSCULUS;
Santos J., Malumbres M., Serrano M.,
Santos J., Malendez B., Perez de Castro I., Malumbres M., Serrano M.,
Pellicer A., Fernandez-Taqueras J.;
"Comparative analysis of the p16(INK4a) and p15(INK4b) DNA sequences
in mouse inbred strains.";
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL: U79633; AAD00230.1; -.
HSSP: P55273; IBDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51 VMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAW 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 GRLPVDLAEELGHRDVARYLRAA-----AGGT--RGSNHARIDAAEGPSDIP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.4%; Score 331; DB 11; Length 113; 60.2%; Pred. No. 1.7e-21; tive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5D4DE8325D06638B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 31, 2001, 07:13:46 Job time: 538 sec
                                                                                                                                                                                                                                                                                                      InterPro; IPR02110; -. Pfam; PF00023; ank; 2. PROSITE; PS50297; ANK_REP_REGION; Kinase; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                           113
12170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 60.2
Matches 68; Conservative
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113 AA;
                           NCBI_TaxID=10090;
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NON_TER
SEQUENCE
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October 31, 2001, 07:02:33; Search time 51.96 Seconds (without alignments) 182.012 Million cell updates/sec
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**SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:**

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**SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:**

**SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:**

**SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:**

**SIDS8/gcgdata/geneseq/geneseqg/geneseqp/AA1999.DAT:**

**SIDS8/gcgdata/geneseq/geneseqg/geneseqp/AA1999.DAT:**

**SIDS8/gcgdata/geneseq/geneseqg/geneseqp/AA1999.DAT:**

**SIDS8/gcgdata/geneseq/geneseqg/geneseqg/geneseqp/AA1999.D
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412676 seqs, 60623988 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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800
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| Description                   | Cell-cycle regulat | Human INK-4 protei | Humman cell cycle r<br>Tumour suppressor | Human multiple tum | Amino acid sequenc | Human MTS1 protein | A human multiple t | Human MTS1 protein | Human p16 protein | Human cyclin depen |
|-------------------------------|--------------------|--------------------|------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|
| SUMMARIES                     | AAR85116           | AAY24741           | AAW10627                                 | AAW19251           | AAW74549           | AAW40524           | AAW80524           | AAB15498           | AAY97524          | AAY96053           |
| DB                            | 16                 | 20                 | 18                                       | 18                 | 19                 | 19                 | 20                 | 21                 | 21                | 21                 |
| å<br>Query<br>Match Length DB | 156                | 156                | 156                                      | 156                | 156                | 156                | 156                | 156                | 156               | 156                |
| %<br>Query<br>Match           | 100.0              | 100.0              | 98.6                                     | 98.6               | 98.6               | 98.6               | 98.6               | 98.6               | 98.6              | 98.6               |
| Score                         | 800                | 800                | 789                                      | 789                | 789                | 789                | 789                | 789                | 789               | 789                |
| Result<br>No.                 | н                  | 7 &                | 4                                        | S                  | 9                  | 7                  | 80                 | 6                  | 10                | 11                 |

|                    |          |          |                    |                    |                    |                    |                    |                   |                    |                   |                    |                   |                    |          |          |          |                    |          |                   |          |                   |                    |                    |                    |          |          |          |                   |                   |                    |                    |          | •                  |
|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|-------------------|--------------------|-------------------|--------------------|----------|----------|----------|--------------------|----------|-------------------|----------|-------------------|--------------------|--------------------|--------------------|----------|----------|----------|-------------------|-------------------|--------------------|--------------------|----------|--------------------|
| Human cyclin depen | multiple |          | Human MTS1 protein | Human multiple tum | Protein encoded by | Human Multiple Tum | Human W9 protein s | Antiproliferative | Angiogenesis inhib | Truncated p27/p16 | Human W9 protein s | Antiproliferative | Angiogenesis inhib | 027      |          | 4        | Anglogenesis inhib |          | Truncated p27/p16 | - 51     | Antiproliferative | Angiogenesis inhib | CDK inhibitory fus | Human p16p27 fusio |          | ب        |          | Antiproliferative | Antiproliferative | Angiogenesis inhib | Anglogenesis inhib | γĒ       | Human p16(GS)p27 f |
| AAY96067           | AAY92921 | AAY91102 | AAY59415           | AAY54902           | AAB67334           | AAB36890           | AAY97522           | AAY96051          | AAY96078           | AAW95105          | AAY97534           | AAY96049          | AAY96076           | AAW95106 | AAY97535 | AAY96050 | AAY96077           | AAY96079 | AAW95103          | AAY97532 | AAY96047          | AAY96074           | AAW23536           | AAW95107           | AAW95096 | AAY97527 | AAY97529 | AAY96042          | AAY96044          | AAY96069           | AAY96071           | AAW23535 | AAW95095           |
| 21                 | 21       | 21       | 21                 | 21                 | 22                 | 22                 | 21                 | 21                | 21                 | 20                | 21                 | 21                | 21                 | 20       | 21       | 21       | 21                 | 21       | 20                | 21       | 21                | 21                 | 18                 | 20                 | 20       | 21       | 21       | 21                | 21                | 21                 | 21                 | 18       | 20                 |
| 156                | 156      | 156      | 156                | 156                | 156                | 156                | 228                | 228               | 228                | 237               | 237                | 237               | 237                | 252      | 252      | 252      | 252                | 323      | 334               | 334      | 334               | 334                | 365                | 365                | 365      | 365      | 365      | 365               | 365               | 365                | 365                | 380      | 380                |
| 98.6               | 98.6     | 98.6     | 8                  | 8                  | œ                  | œ                  | 8                  | ω.                | ω.                 | æ                 | 8                  | œ                 | 0                  | ъ.       | ω.       | 8        | θ.                 | ω.       | ω,                | æ        | œ                 | œ                  | æ                  | ъ<br>Ж             | ъ<br>Э   | æ        | о<br>О   | ъ<br>Э            | æ                 | ъ<br>Э             | ъ.                 | 90       | æ                  |
| 789                | 789      | 789      | $\infty$           | œ                  | œ                  | œ                  | œ                  | œ                 | œ                  | œ                 | œ                  | æ                 | æ                  | œ        | œ        | œ        | œ                  | œ        | æ                 | œ        | œ                 | 788                | æ                  | æ                  | œ        | æ        | 788      | œ                 | œ                 | œ                  | 788                | œ        |                    |
| 12                 | 13       | 14       | 15                 | 16                 | 17                 | 18                 | 19                 | 20                | 21                 | 22                | 23                 | 24                | 25                 | 26       | 27       | 28       | 29                 | 30       | 31                | 32       | 33                | 34                 | 35                 | 36                 | 37       | 38       | 39       | 40                | 41                | 42                 | 43                 | 44       | 45                 |

## ALIGNMENTS

New cell cycle regulating proteins bind to cyclin dependent kinase

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Serrano M,
                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                              AAY88354 standard; Protein; 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92US-0991997.
93US-0154915.
94US-0227371.
94US-0248812.
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                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                               Matches 156; Conservative
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                                                                                                                                                                      Similarity
                                                                                                                                 156 AA
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25-MAY-1994;
14-SEP-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (COLD-) COLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JAN-1996;
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30-JUN-1995;
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                                                                                                                                  Sequence
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                                             The human cell-cycle regulatory (CCR) protein p16 (AAR85116) was obtd. by expression of a cDNA clone (AAT02962) isolated in a 2 hybrid screening assay. CCR p16 specifically inhibits the activity of cyclin-dependent kinases during various stages of the cell cycle, and can be used in the treatment and diagnosis of proliferative
                                                                                                                                                                                                                              61 elllihgaepncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaee 120
                                                                                                                                                                                                                     ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                              Gaps
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and related nucleic acids, antibodies etc., used in diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                       INK-4; p16; p15; p18; p19; CDK4; cell cycle regulatory protein;
transgenic mouse; p16-INK4-a; carcinogen; anti-proliferative.
                                                                                                                                                             0;
                                                                                                                                           Length 156;
                                                                                                                                                              Indels
         therapy of abnormal cell proliferation, degeneration etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic mice with modified cell-cycle regulation
                                                                                                                                          100.0%; Score 800; DB 16; 100.0%; Pred. No. 4.6e-86;
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                                                                                                                                                                                                                                                                    LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 45-46; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (COLD-) COLD SPRING HARBOR LAB. (YESH ) UNIV YESHIVA EINSTEIN COLLEGE.
                            English.
                                                                                                                                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                           AAY24741 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0627610.
93US-0154915.
94US-0227371.
94US-0208812.
94US-0346147.
95US-0497214.
                          Page 76-77; 109pp;
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                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Human INK-4 protein p16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-394656/33.
N-PSDB; AAX80472.
                                                                                                                                                     Similarity
                                                                                                               156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1994;
29-NOV-1994;
30-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5919997-A.
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14-APR-1994;
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                                                                                                                                                     Local Sim
hes 156;
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Best Local S
Matches 156
                                                                                              disorders
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                            Claim 1;
                                                                                                                 Sequence
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ó The present invention describes a transgenic mouse having germline and somatic cells which comprise an incorporated transgene that disrupts and inhibits the pi6-INK4-a gene leading to tumour susceptibility. Also described is a method of making a mouse and mouse embryonic stem cells a functionally disrupted pl6-INK4-a gene which comprises transferring a transgene construct into embryonic stem cells of a mouse and transferring these into a mouse blastocyst and implanting the resulting chimeric blastocyst into a female mouse selecting offspring having an endogenous p16-INK4-a gene allele. The transgenic mouse is useful for evaluating the carcinogenic potential or the anti-proliferative activity of a test compound. The present sequence represents the human INK4 Cell cycle regulatory protein; CCR; p16; diagnostic assay; detection; cell proliferation; differentiation; neoplasia; cancer; cell growth; cyclin-dependent kinase inhibitor; CDK; human; chromosome 9p21-22. 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120 Gaps 9 Use of a mammalian cell cycle regulatory protein (a CDK-inhibitory protein) in a diagnostic assay for identifying a cell at risk for a 1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 0 Length 156; Human cell cycle regulatory protein p16 amino acid sequence. Indels DB 20; 0 Hannon GJ; 100.0%; Score 800; DB 20; 100.0%; Pred. No. 4.6e-86; ive 0; Mismatches 0; protein p16 given in the present invention

Jin X, Roth J;

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This sequence represents the human cell cycle regulatory protein (CCR) pl6 amino acid sequence. The pl6 qene is located on chromosome 9p21-22. The invention relates to a diagnostic assay which comprises detecting a risk of developing a disorder characterised by unwanted cells at risk of developing a disorder characterised by unwanted cell or cells at confideration or differentiation. Pl6 is a cyclin-dependent kinase comprises and ultimately cell growth. The assay can be used for identifying a cell or cells at risk for a disorder (neoplasia) characterized by unwanted cell growth. The assay can be used for characterized by unwanted cell proliferation or differentiation. The method is used for detecting mutations in either a CCR gene or CDK gene which alter complex formation between these two proteins which also used for detecting mutations in other cellular proteins which disrupt protein interactions such as mutations which disrupt binding of the p53 protein with other cellular proteins which disrupt brotein with other cellular proteins which pairs of signal transduction proteins such as ras protein or other cellular proteins (GARPS). The method is such as ras protein or other cellular proteins which have such as ras protein or other cellular proteins which have seen as a grease activating general proteins which are unable to physically interact with a general convenient for detecting mutants of CCR genes encoding proteins which are unable to physically interact with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppressor; p16; inhibitor; cyclin-dependent kinase 4; CDK4; cancer cell; lung cancer; bladder cancer; melanoma; restenosis; therapy; anti-angiogenic activity; hyperproliferative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
disorder characterized by unwanted cell proliferation or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 800; DB 21; 100.0%; Pred. No. 4.6e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                        Claim 14; Column 57-58; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW10627 standard; Protein; 156 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0502881.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour suppressor p16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDK bait protein.
                    differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-11995;/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUL-11996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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  SSSSSXS
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                                                                                                                                                                                                                                                                                                       This sequence represents the tumour suppressor p16. The DNA encoding this sequence is joined to a promoter functional in eukaryotic cells and used in the expression construct of the invention. p16 is an inhibitory subunit, which is involved in the control of cyclin-dependent kinase 4 activity, and functions as a tumour suppressor. By detecting this sequence or the DNA encoding it, cancer cells can be detected. When the nucleic acid molecule is in the sense orientation, the expression construct can be used to restore p16 function in a cell, particularly by the expression of the expr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bladder cancer or melanoma. It may also have anti-angiogenic activity, and inhibit hyperproliferative disorders, e.g. restenosis. When the nucleic acid molecule is inserted in the antisense orientation, the expression construct inhibits plb function. Reduced or increased levels of pl6, or a related nucleic acid, may be diagnostic of tumours, e.g. by Southern or Northern blot, antibody immunoblot, fluorescent cell sorting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 elllhgaepncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaee 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Expression construct contg. DNA for tumour suppressor p16 - to restore p16 activity to transformed cells, useful for treating lung or bladder cancer or melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 789; DB 18; Length 156;
Pred. No. 8.9e-85;
1; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; multiple; tumour; suppressor; MTS1; cancer; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human multiple tumour suppressor 1 gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 1b; 92pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW19251 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.68;
98.78;
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94US-0215086.
94US-0215087.
94US-0227369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 98.7
Matches 154; Conservative
                                                WPI; 1997-132336/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 156 AA;
                                                                              N-PSDB; AAT60951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or immunoassay.
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18-MAR-1994;
18-MAR-1994;
14-APR-1994;
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AAW19251
δλ
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MTS1; multiple tumour suppressor; diagnosis; cancer; germ-line mutation; familial melanoma locus; MLM; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of the multiple tumour suppressor I (MTS-1) protein, used in the method of the invention. The MTS gene is useful in the diagnosis and prognosis of human cancer, e.g. by standard nucleic hybridisation techniques, of patient samples. The mutated sequences are those that are present in somatic mutations of the gene in cancers. The vectors can be used for gene therapy strategies to replace function of mutated protein in patients. These can also be used to construct protein mimetics, also for therapeuttc strategies. In addition the expression constructs can also be used for recombinant production of MTS. Recombinant MTS can be used to screen for drugs to be used for cancer therapy, and the protein itself may also be used to restore MTS function in a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                Nucleic acids based on multiple tumour suppressor, MTS, sequences useful as hybridisation probes, primers and recombinant production of MTS in the diagnosis and treatment of cancers related to MTS
                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                              Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                            Score 789; DB 19; Dred. No. 8.9e-85; 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 63-64; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW40524 standard; Protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                              98.6%;
98.7%;
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94US-0215087.
94US-0227369.
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95WO-US03316.
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Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MTS1 protein.
                                                                                                                                                                                                                                                                                                                                                               156 AA;
 N-PSDB; AAV53819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
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17-MAR-1995;
                                                                                    mutation(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW40524;
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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AAW40524
     δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Multiple tumour suppressor 1; MTS-1; human; cancer; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                  - for
                                                                                                                                                                                                                                                                                                                                                                Length 156;
                                                                                                                                                                                                                                                             The present sequence the human multiple tumour suppressor (WTS1) gene product, useful in cancer diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                 Human mutant multiple tumour suppressor gene sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of multiple tumour suppressor 1.
                                                                                                                                                                                                                                                                                                                                                             Query Match 98.6%; Score 789; DB 18; Best Local Similarity 98.7%; Pred. No. 8.9e-85; Matches 154; Conservative 1; Mismatches 1;
                                                                                                                                                                                              production of recombinant mutant polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 lghrdvarylraaaggtrgsnharidaaegpsdipd 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                 Skolnick MH;
                                                                                                                                                                                                                             Claim 1; Columns 61-64; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW74549 standard; Protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      somatic mutation; gene therapy.
                                                                                                 Kamb A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0214582.
94US-0215086.
94US-0215087.
 94US-0251938
95WO-US03537
                                                (MYRI-) MYRIAD GENETICS INC
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95WO-US03316
                                                                 UNIV UTAH RES FOUND
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                                                                                                 Cannon-Albright LA,
                                                                                                                              WPI; 1997-258217/23.
N-PSDB; AAT72311.
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                                                                                                                                                                                                                                                                                                               156 AA;
01-JUN-1994;
17-MAR-1995;
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18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
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                                                                                                                                                                                                                                                                                                              Sequence
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                                                                 (UTAH)
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This sequence represents the human multiple tumour suppressor 1 (MTS1) amino acid sequence. The protein has a cytostatic activity and is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel protein composition useful in protein replacement therapy for diagnosing and treating cancer comprises a specific weight percent of human multiple tumour suppressor 1 polypeptide .
                                                                                                                                                                                                                                                                                                                                          ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human multiple tumour suppressor 1 (MTS1) protein. The sequence is homologous to the corresponding murine gene. Primers designed from the gene can be used to design primers to detect abnormalities i.e. polymorphisms which may predispose towards malignancies such as melanoma, leukaemia, as astrocytoma, lymphoma, glioma, as well as tumours of e.g. the breast, thyroid, pancreas, uterus and kidneys.
                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                            1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; human; multiple tumour suppressor 1; MTS1; diagnostic; cancer; gene therapy; protein replacement therapy.
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                          Length 156;
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                      Score 789; DB 20;
Pred. No. 8.9e-85;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                               121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
95WO-US03316.
                                                                                                                                                                                                      Ouery Match 98.6%;
Best Local Similarity 98.7%;
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-0480810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MTS1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAA95633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MYRI-) MYRIAD
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18-MAR-1994;
18-MAR-1994;
14-APR-1994;
14-APR-1994;
01-JUN-1994;
17-MAR-1995;
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                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB15498;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB15498
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                                                                                                                                                                               This sequence represents a human multiple tumour suppression protein, MTS1. The MTS gene locus is also referred to as the familial melanoma (MLM) gene locus, located on human chromosome 9p21. Germ line mutations in MTS genes can be used in the diagnosis of predisposition to cancers, e.g. melanoma, leukaemia, astrocytoma, gliboblastoma, lymphoma, glioma, Hodgkin's lymphoma, CLL, and cancers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, stomach and rectum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELLLIHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse multiple tumour suppressor gene segment - useful for primer
                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                           Length 156;
                                                                               DNA specific for Multiple Tumour Suppressor IEI-beta gene useful for the diagnosis of cancers related to MTSIEI-beta mutation(s) and their treatment
                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; multiple tumour suppressor 1 gene; MTS1; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A human multiple tumour suppressor 1 (MTS1) protein.
                                                                                                                                                                                                                                                                                                                                                                          Score 789; DB 19;
Pred. No. 8.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Columns 65-66; 80pp; English.
                                                                                                                                                 Disclosure; Column 63-64; 72pp; English.
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98.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                        Matches 154; Conservative
                              WPI; 1998-250421/22.
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamb A,
                                               N-PSDB; AAV11238
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                                                                                                                                                                                                                                                                                                                      156
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                      Sequence
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Kamb A;
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The invention relates to a protein composition comprising a novel purfised commercial expendent kinase inhibitor (CDKi) and a purified adenovirus E4 protein. The compositions comprising the protein, or the DNA encoding it are useful for treating neoplasias in animals. The
protein replacement therapy. MTS1 is useful in diagnosing human cancers such as (ocular) melanoma, leukemia, astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma, multiple myeloma, sarcoma, myosarcoma, cholangiocarcinoma, squamous cell carcinoma, CLL, and cancers of pancreas, breast, stomach, brain, prostate, bladder, thyroid, ovary, uterus, testis, kidney, colon and rectum. The MTS1 gene and protein is useful in gene therapy, protein replacement therapy and protein mimetic
                                                                                                                                                                                                                            61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                   Gaps
                                                                                                                                                                       9
                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein and nucleic acid compositions for preventing and treating neoplasias (particularly cancer), comprises a novel chimeric cyclin dependent kinase inhibitor and adenovirus E4 protein -
                                                                                                                                                                                   1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA
                                                                                                                                                                                                                                                                                                                                                                                                                    Human; chimeric cyclin dependent kinase inhibitor; CDKi; therapy; adenovirus E4 protein; neoplasia; p16 protein.
                                                                                                                                                  0;
                                                                                                                             Length 156;
                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Finer
                                                                                                                            Score 789; DB 21;
Pred. No. 8.9e-85;
                                                                                                                                                                                                                                                                     Mendez MJ,
                                                                                                                                                                                                                                                          121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 123; 126pp; English.
                                                                                                                                                                                                                                                                                                                                  AAY97524 standard; Protein; 156 AA
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                                                                                                                            98.68;
98.78;
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99US-0128515.
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                                                                                                                                                                                                                                                                                                                                                                                                Human p16 protein sequence
                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CELL-) CELL GENESYS INC
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                                                                                                                                        Similarity
                                                                                               156 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                  Matches 154;
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                                                                                                Sednence
                                                                                                                               Query Match
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                                                                            studies
                                                                                                                                         Local
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compositions also find use in assays to eliminate a specific sub-population of cultured cells, to determine the susceptibility of neoplastic cells to treatment with the compositions and also in assays synchronise cell growth in cultured cells.
                                                                                                                                                                                                                                                                                                                                                                                                                         61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       elllihgaepncadpatltrpvhdaaregfidtlvvlhragarldvrdawgrlpvdlaee 120
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                                                                                                                                                                                                                                                                                                                                                    1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA
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                                                                                                                                                                                                                Length 156;
                                                                                                                                                                                                              ; DB 21;
8.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cyclin dependent kinase inhibitor p16.
                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                Score 789;
                                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                                98.6%;
98.7%;
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99US-0163682.
99US-0457568.
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                                                                                                                                                                                                                   Query Match 98.6
Best Local Similarity 98.7
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-594183/56.
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                                                                                                                                   156 AA;
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09-DEC-1999;
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                                                                                                                                         Sequence
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18-MAR-1994;
18-MAR-1994;
18-MAR-1994;
14-APR-1994;
01-JUN-1994;
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                                                                                                                                                                                  Query Match
                                                                                                                                                                                             Local
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fragments of these, or fusion proteins comprising (active fragments of) an INK4 family protein and a CIP/KIP family protein (see AAY96046 and AAY96049). The method is used to inhibit mammalian smooth muscle cell hyperproliferation induced by injury caused by angioplasty, stent placement or vein engraftment. It is useful for treating vascular pathologies, e.g. restenosis. Also claimed are recombinant lentiviruses encoding CDKis.
                                                                                                                                                                                                            ellllhgepncadpatltrpvhdaaregfldtlvvlhragarldvrdawgrlpvdlaee 120
                                                                                                                                                                                               61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                        Gaps
                                                                                                                                                                   1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting angiogenesis and treating angiogenesis-associated conditions, e.g. neoplasia, psoriasis by transducing an endothelial cell with a recombinant virus having a transgene encoding a cyclin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of human p16, a cyclin dependent kinase inhibitor (CDKi) that inhibits angiogenesis. A claime
                                                                                                                                                                                                                                                                                                                                                                                                Cyclin dependent kinase inhibitor; CDKi; INK4; human; p16; angiogenesis; inhibitor; neoplasia; rheumatoid arthritis; endometriosis; psoriasis; vascular retinopathy; cytostatic; antiarthritic; antirheumatic; gynaecological; antipsoriatic;
                                                                                                                 Length 156;
                                                                                                                                      Indels
                                                                                                                Score 789; DB 21;
Pred. No. 8.9e-85;
1; Mismatches 1;
                                                                                                                                                                                                                                                   LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                               Human cyclin dependent kinase inhibitor p16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 129; 138pp; English.
                                                                                                                                                                                                                                                                                                                    Ą.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gyuris J;
                                                                                                                                                                                                                                                                                                                 AAY96067 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                          antiproliferative; gene therapy
                                                                                                                98.68;
98.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000WO-US04970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0122974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0163682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dependent kinase inhibitor
                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                          Best Local Similarity 98.7
Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CELL-) CELL GENESYS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mcarthur J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-565501/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MITO-) MITOTIX INC
                                                                                   156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA50520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200052158-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-NOV-1999;
09-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-2000
                                                                                                                                                                                                                                                                                                                                     AAY96067;
                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patel S,
                                                                                                                Query Match
                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                        AAY96067
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ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Variant; human; multiple tumour suppressor; MTS; mutation; melanoma;
method for inhibiting anglogenesis involves transducing an epithelial cell with a transgene encoding (internalizable, secretable) CDKi. The delivery system for the transgene may be a liposome or a recombinant virus. The CDKi is preferably a protein of the CIP/KIP family such as p27, a protein of the INK4 family such as p27 and p16 (see AAY96068-80). The method is UDKi proteins such as p27 and p16 (see AAY96068-80). The method is useful in treating conditions associated with anglogenesis, e.g. neoplasia, rheumatoid arthritis, endometriosis, psoriasis and vascular retinopathy (claimed). Alternatively, the transgene is that the CDKi is released into the blood and contacts the target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 789; DB 21;
Pred. No. 8.9e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human multiple tumour suppressor 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY92921 standard; Protein; 156 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.6%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0214582
94US-0215086.
94US-0215087.
94US-0227369.
94US-0251938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0480810.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0120130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95WO-US03316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-269915/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                         156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; diagnosis
                                                                                                                                                                                                                                                                                                                                   epithelial cell.
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18-MAR-1994;
14-APR-1994;
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                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY 59415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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δλ
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0
                        The invention relates to variants (AAA11196-A11206) of the human multiple tumour suppressor 1 (MTS1) protein of which this sequence represents the wild type sequence. The variants have the following changes relative to the wild type coding sequence: A at any of positions 265, 442, 330 and 329; T at any of positions 172, 238, 341 and 148 and deletions of nucleotides 290-294, 172-179 or 128-129. The variants are sommatic mutations of MST1, indicative of predisposition to melanoma and many other cancers, so detecting them is useful for diagnosis, prognosis and monitoring of cancer (including prenatal analysis). Cells and animals that express the variants are useful as model systems for identifying potential anticancer agents.
                                                                                                                                                                                                                                                                              61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                          1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; multiple tumour suppressor; MTS; somatic mutation; cancer; diagnosis; germ line mutation; gene therapy; cytostatic; melanoma; leukaemia; astrocytoma; glioblastoma; lymphoma; glioma;
                                                                                                                                                                                                       .;
0
                                                                                                                                                                                 Length 156;
                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human multiple tumour suppressor MTS1 SEQ ID NO:2.
                                                                                                                                                                                 98.6%; Score 789; DB 21; 98.7%; Pred. No. 8.9e-85;
                                                                                                                                                                                                                                                                                                          121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                                                                                                                                                    1; Mismatches
         Disclosure; Column 61-62; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                               AAY91102 standard; Protein; 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               950S-0480810.
970S-0986147.
940S-0215086.
940S-0215087.
940S-0215087.
94US-0251938.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0115252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                        154; Conservative
                                                                                                                                                                                   Ouery Match
ast Local Similarity
tches 154; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-349676/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hodgkin's lymphoma.
                                                                                                                                                     156 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA39353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6060301-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
08-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAR-1994
18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                    AAY91102;
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kamb A;
                                                                                                                                                                                                                                                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                      AAY91102
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The present invention describes a vector (1) comprising an isolated DNA sequence of a multiple tumour suppressor (MTS) gene having a sequence of a multiple tumour suppressor (MTS) gene having a polynucleotide sequence of the human MTSIE1-beta. (1) is useful for introducing wild-type MTS function to a cancerous or pre-cancerous cell which carries diminished or mutant MTS alleles for suppressing cell which the mutant gene is expression of MTS gene even in tumour cells in which the mutant gene is expressed at a normal level but the gene product is not fully functional. A host cell transformed with (1) is useful as a model system to study cancer remission and drug treatment which promotes such remission. The present invention relates to somatic mutations and germ line mutations in the MTS gene and their use in the diagnosis and prognosis of human cancer e.g. melanoma, leukaemia, astrocytoma, alloblastoma, lymphoma, alloma, Hodgkin's lymphoma, accomers of the pancreas, breast, thyroid, ovary, uterus, testis, kidney, scomach and rectum. The present sequence represents human MTSI, which is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or useful for gene therapy of cancer associated with mutation suppressor gene, comprises DNA sequence of multiple tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                  Disclosure; Column 63-64; 71pp; English.
          New vector useful for gene therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY59415 standard; Protein; 156 AA
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94US-0215086.
94US-0215087.
94US-0227369.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0848251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 98.7
Matches 154; Conservative
                                                                                suppressor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; MTS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1994;
18-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5989815-A.
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This sequence represents the human MTSI protein.

The invention relates to a method for diagnosing a polymorphism
associated with a predisposition to cancer by detecting a germ-line
alteration of a wild-type Multiple Tumour Suppressor (MTS) gene or its
expression products in a human sample. The method comprises detecting a
germ-line alteration of a wild-type MTS gene or its expression products
in a human sample, the alteration indicating a predisposition to at least
one of the cancers. The cancer is selected from melanoma, leukaemia,
astrocytoma, glioblastoma, lymphoma, glioma, Hodgkin's lymphoma,
chronic lymphocytic leukaemia (CLL), and cancers of the pancreas, breast,
thyrold, ovary, uterus, testis, kidney, stomach and rectum. The method
may be used as the basis for developing very important diagnostic tests
capable of predicting the predisposition to cancer. The MTS gene is
involved in the progression of multiple tumour types and may provide
means for a general anti-cancer therapy by virtue of its ability to
                                                                                                                                                                                                                                      Diagnosing a polymorphism associated with a predisposition for cancer
                                                                                                                                Kamb A;
                                                                                                                                                                                                                                                                                   Claim 1; Column 61-64; 74pp; English.
                                                                                                                                Skolnick MH, Cannon-Albright LA,
94US-0251938
95WO-US03537
                                                                 (UTAH ) UNIV UTAH RES FOUND (MYRI-) MYRIAD GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          suppress tumour growth.
                                                                                                                                                                         WPI; 2000-070785/06.
N-PSDB; AAZ48770.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156 AA;
  01-JUN-1994;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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; ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120 0; Gaps 1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60 Query Match 98.6%; Score 789; DB 21; Length 156; Best Local Similarity 98.7%; Pred. No. 8.9e-85; Matches 154; Conservative 1; Mismatches 1; Indels ( Query Match 61 q δ ò

LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156 121

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Search completed: October 31, 2001, 07:03:38 Job time: 65 sec

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Sequence 1 Sequence 1 Sequence 1 Sequence 1

Sequence Sequence Sequence Sequence

sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 8, Al Sequence 8, Al Sequence 8, Al

Sequence

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1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08627610
Patent No. 591997
GENERAL INFORMATION:
APPLICANT: Berrano, Manuel
APPLICANT: Serrano, Manuel
APPLICANT: Depinho, Ronald A.
TITLE OF INVENTION: Transgenic Animals Having Modified Cell-Cycle
TITLE OF INVENTION: Regulation
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 800; DB 2; 100.0%; Pred. No. 1.6e-87;
US-08-581-918A-12
US-08-346-147B-12
US-08-487-033-14
US-08-480-810-14
US-08-848-735-14
US-08-848-735-14
US-08-948-735-14
US-09-115-252-14
US-09-115-252-14
US-09-120-129-14
US-09-120-139-14
US-09-201-139-14
US-09-201-139-14
US-09-201-131-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CSI-001CP6
TELECOMUNICATION INFORMATION:
TELEPONE: (617) 227-7400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/627,610
FILING DATE: 04-APR-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-627-610-2
   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
     USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 60 St
CITY: Boston
                     Q
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 CITY: E
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58.487 Million cell updates/sec
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                                                                                                                Search time 54.92 Seconds
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Sequence 2,
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1 MDPAAGSSMEPSADWLATAA......TRGSNHARIDAAEGPSDIPD
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcayCOMB.pep:*
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08 893-741-2
US-08-893-741-2
US-08-81-918A-2
US-08-822-936-2
US-08-822-936-2
US-08-10-2
US-08-10-2
US-08-10-2
US-08-10-2
US-08-10-2
US-08-10-2
US-08-10-2
US-08-10-2
US-08-10-120-2
US-09-120-139-2
US-09-120-139-2
US-09-120-139-2
US-09-120-139-2
US-09-120-139-2
US-09-120-131-2
US-08-910-131-2
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PCT-US93-09945-4
                                                                                                                                                                                                                                                                                                  197339 seqs, 20590346 residues
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                                                                                                              October 31, 2001, 07:02:33
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB
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GENERAL INFORMATION:
Patent No. 5968821
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STATE:
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                   61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                             Sequence 2. Application US/08306511A

Patent No. 5962316

GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Beach, David H.
APPLICANT: Bennon, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatry Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0; Indels
                                                                                                                       121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,511A
FILING DATE: 14-5EP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRENCE/DOCKET NUMBER: CSI-001CP2
REFERENCE/DOCKET NUMBER: CSI-001CP2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 227-7400
TELEFAX: (617) 227-7401
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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US-08-306-511A-2
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US-08-893-274-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                          APPLICANT: Serrano, Manuel Applicant: Serrano, Manuel Tapplicant: Hannon, Gregory J. TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, TITLE OF INVENTION: and Uses Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 800; DB 2;
100.0%; Pred. No. 1.6e-87;
iive 0; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812

FILING DATE: 25-WAY-1994

PRIOR APPLICATION NUMBER: US 08/227,371

FILING DATE: 14-APRIL-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915

FILING DATE: 18-NOVEMBER-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,997

FILING DATE: 17-DECEMBER-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCTOBER-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,308

FILING DATE: 16-OCTOBER-1992

ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,274
FILING DATE: 15-JULY-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEPTEMBER-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.09
TELECOMMUNICATION INFORMATION:
                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: Beach, David H. APPLICANT: Demetrick, Douglas J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 156 amino acids
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Best Local Similarity 100.
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein US-08-893-274-2
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                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                         Boston
                                                                                                                                                                                                                                                                                   COUNTRY: US
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Wed Oct 31 07:17:17 2001
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ADDRESSEE:

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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE
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APPLICANT: Beach.
APPLICANT: Beach.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 800; DB 4; Length 156; Pred. No. 1.6e-87;
                                                                                                                                                                   121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
                                                                                                                                                                                            PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAY-1994
PROR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Vincent, Matthew P.
REGISTATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/346,147B
FILING DATE: 29-NOV-1994
CLASSIFICATION: 514
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STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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100.0%;
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TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 17-DEC-1992 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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US-08-346-147B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02109
                                                                                                                                                                                                                                                                                RESULT 5
US-08-346-147B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Beach, David H.
APPLICANT: Demetrick, Douglas J.
APPLICANT: Serrano, Manuel
APPLICANT: Hannon, Gregory J.
TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and Uses
TITLE OF INVENTION: Related Thereto
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 156;
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Pred. No. 1.6e-87;
121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDERS CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,918A
FILING DATE: 02-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/497,214
FILING DATE: 30-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/346,147
FILING DATE: 29-NOV-1994
PRIOR APPLICATION NUMBER: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-071.06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/248,812
FILING DATE: 25-MAX-1994
APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/227,371
FILING DATE: 14-APR-1994
APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/154,915
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/991,997
FILING DATE: 17-DEC-1992
ATTORNEY/AGENT INFORMATION: NAME: Vincent, MATCHEW P.
REGISTRATION NUMBER: 36,709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                          RESULT 4
US-08-581-918A-2
: Sequence 2, Application US/08581918A
; Patent No. 6043030
                                                                                                                                                                                                                                                                                                                                                               E: Foley, Hoag & Eliot
One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (617) 832-1299
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 156 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                    STREET: One PC
CITY: Boston
STATE: MA
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ZIP: 02109
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TOPOLOGY: LENGTH:

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61 ELLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell-Cycle Regulatory Proteins, and Uses
Related Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 156;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew STREET: One Market Plaza, Steuart Street Tower CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 800; DB 5; 100.0%; Pred. No. 1.6e-87;
121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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CLASSIFICATION:
CLASSIFICATION DATA:
APPLICATION NDARE:
ILING DATE: 20-NOV-1994
PRIOR APPLICATION NDARE: 08/306,511
FILING DATE: 14-SEP-1994
PRIOR APPLICATION NDARE: 08/248,812
FILING DATE: 25-NAY-1994
PRIOR APPLICATION NDARE: 08/248,812
FILING DATE: 25-NAY-1994
PRIOR APPLICATION NDARE: 08/248,812
FILING DATE: 14-APR-1994
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04636
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                Sequence 2, Application PC/TUS9504636 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application PC/TUS9605252 GENERAL INFORMATION:
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amino acid
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CE
                                                                                                             RESULT 7
PCT-US95-04636-2
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APPLICANT: Massague, Joan
APPLICANT: Roberts, James M.
APPLICANT: Roff, Andrew
APPLICANT: Rolf, Andrew
APPLICANT: Andrew
APPLICANT
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                                                                                                                 1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMGSARVA 60
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   Indels
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ZIP: USA
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.25
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,936
FILING DATE: 21-FEBRUARY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-079.05
TELEDHONE: (617) 832-1000
TELEPHONE: (617) 832-1000
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Best Local Similarity 100.0%; Pred. No. 1.6e-87;
Matches 156; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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   Mismatches
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Patent No. 6242575
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amino acid
   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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Matches 156;
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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08487033
Patent No. 5739027
GENERAL INFORMATION:
ADPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSIEL-Beta GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY, Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 3.3e-86;
1; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24884-109348-E
                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.6%;
98.7%;
     07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-962-4810
TELEFAX: 202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-962-8300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , MOLECULE TYPE: protein US-08-474-177-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-487-033-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALDNAPNSYGRRPIQVMMGSARVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 157;
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Patent No. 5624819
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kanh, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP STREET: 1201 New York Avenue, Suite 1000
CITY: Waghington
                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05252 FILING DATE: Not yet assigned CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/425,093
FILING DATE: 17-APR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 789.5; DB 5;
Pred. No. 2.9e-86;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                                                             02307B-059910PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION: 1..157
; OTHER INFORMATION: /note= "human pl6"
PCT-US96-05252-5
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                               NAME: Weber, Ellen L.
REGIGSTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.7%;
                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                            157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.49
Matches 156; Conservative
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.6%; Score 789; DB 1; Length 156; 98.7%; Pred. No. 3.3e-86;
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Patent No. 5843756
GENERAL INFORMATION:
APPLICANT: Stone, Steven
APPLICANT: Jiang, Ping
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTS GENE AND THERAPEUTIC USE THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDR
                                                  PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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1; Mismatches
                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 17-MAR-1995
PRIOR DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
ATTORNEY, AMERICATION:
AMANE: THORNEY, AMERICATION:
AMANE: THORNEY, AMERICATION:
AMANE: THORNEY, AMERICATION:
AMANE: THORNEY, AMANE: THORNEY, THORNE
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                                                                                                                                 UMBER: US/08/480,810
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
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                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 98.7
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 156 amino acids
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MOLECULE TYPE: protein
US-08-480-810-2
                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                             FILING DATE:
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STATE: DO
COUNTRY:
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98.7%; Pred. No. 3.3e-86;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08480810
Patent No. 5801336
GENERAL INFORMATION:
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: MTSI GENE
NUMBER OF SEQUENCE: 36
CORRESSEDNDENCE ADDRESS:
ADDRESSE: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                   CLASSITICATION DATA:

CLASSITICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

FILING DATE: 17-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/251,938

FILING DATE: 01-JUN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,087

FILING DATE: 18-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/215,086

FILING DATE: 18-MAR-1994

PRIOR APPLICATION NUMBER: US 08/227,369

FILING DATE: 18-MAR-1994

PRIOR APPLICATION NUMBER: US 08/227,369

FILING DATE: 18-MAR-1994

PRIOR APPLICATION NUMBER: US 08/214,582

FILING DATE: 18-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Thnen, Jeffrey L.

REGISTRATION UMBER: 28,957
                                                  APPLICATION NUMBER: US/08/487,033
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.6
Best Local Similarity 98.7
Matches 154; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-487-033-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
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1 MDPAAGSSMEPSADWLATAAARGRVEEVRALLEAVALPNAPNSYGRRPIQVMMMGSARVA 60
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Patent No. 5994095
GENERAL INFORMATION:
APPLICARM: Kamb, Alexander
TITLE OF INVENTION: MTS2 GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSES: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD 156
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                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/03537
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,087
FILING DATE: 18-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/215,086
FILING DATE: 18-MAR-1994
PRIOR APPLICATION NUMBER: US 08/215,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/217,369
FILING DATE: 14-APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
APPLICATION NUMBER: US 08/214,582
FILING DATE: 18-MAR-1994
                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/474,083
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: PCT/US95/03537
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/848, 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Innen, Jeffrey L. REGISTRATION NUMBER: 28,957 REPERENCE/DOCKET WUNBER: 246 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 98.7%
Matches 154; Conservative
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MOLECULE TYPE: protein
US-08-848-251-2
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COMPUTER READABLE FORM:
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US-08-486-047-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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APPLICANT: SKOLDICK, MARK H.
APPLICANT: Cannon-Albright, Lisa A.
APPLICANT: Kamb, Alexander
TITLE OF INVENTION: GERMLINE MUTATIONS IN THE MTS GENE AND
TITLE OF INVENTION: METHOD FOR DETECTING PREDISPOSITION TO CANCER AT THE MTS
TITLE OF INVENTION: GENE
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.6%; Score 789; DB 2; Length 156; 98.7%; Pred. No. 3.3e-86; Live 1; Mismatches 1; Indels
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   COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,735
FILING DATE:
CLASSTRATE.
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                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PREDE CLASSIFICATION OBTER: US to be assigned
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US95/03316
FILING DATE: 17-MAR-1995
ATTORNEY, AGENT INFORMATION:
NAME: Inhen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24,884
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OFFICE 
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Patent No. 5989815
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LENGTH: 156 amino acids
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Best Local Similarity 98.7
Matches 154; Conservative
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; MOLECULE TYPE: protein
US-08-508-735-2
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US-08-848-251-2
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US-09-120-130-2
| Sequence 2, Application US/09120130
| Sequence 2, Application US/09120130
| Patent No. 6037462
| GENERAL INFORMATION: Ramb, Alexander APPLICANT: Ramb, Alexander TITLE OF INVENTION: MTS1 GENE NUMBER OF SEQUENCES: 36
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: ADDRESSE: CITY: Washington STATE: DC
| CTY: Washington STATE: DC
| COUNTRY: USA
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                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

PELLOR DATE:

CLASSIFICATION NUMBER:

CLASSIFICATION NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

PILING DATE:

17-WAR-1995

PRIOR APPLICATION DATA:

APPLICATION UNBER:

PILING DATE:

17-WAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

AND ANTA:

APPLICATION NUMBER:

ATTORNEY AGENT INFORMATION:

ANAME:

AN
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REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109348-B
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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61 ELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEE 120
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALEARIT RE-Lease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,130
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98.7%; Pred. No. 3.3e-86;
tive. 1; Mismatches 1.
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                                                                                                                                                                                                                                                                FILING DATE:
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/251,938
FILING DATE: 01-UN-1994
PRIOR APPLICATION DATE: US 08/251,938
FILING DATE: 10-UN-1994
PRIOR APPLICATION NUMBER: US 08/215,087
FILING DATE: 18 WAR-1994
PRIOR APPLICATION NUMBER: US 08/215,086
FILING DATE: 18 WAR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14 APR-1994
PRIOR APPLICATION NUMBER: US 08/227,369
FILING DATE: 14 APR-1994
PRIOR APPLICATION NUMBER: US 08/214,582
RILING DATE: 18 WAR-1994
FILING DATE: 18 WAR-1994
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CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE-POCKET NUMBER: 24,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO: 2:
SEGUENCE CHARACTERISTICS:
LENGTH: 156 amino acids
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Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-120-130-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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